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(54) Title: COMPOSITION AND METHOD FOR *IN VIVO* IMAGING OF AMYLOID DEPOSITS

## (57) Abstract

An amyloid binding composition for *in vivo* imaging of amyloid deposits comprising a labeled amyloid protein or variant thereof which binds to amyloid deposits *in vivo*; and a pharmaceutically acceptable carrier, is described. Methods of detecting amyloid deposits and for diagnosing Alzheimer's Disease and Down's Syndrome are also described.

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5                   COMPOSITION AND METHOD FOR IN VIVO IMAGING OF AMYLOID  
                  DEPOSITS

Background of the Invention

10                  The present invention relates to the identification of compositions which are suitable for use in in vivo imaging of amyloid deposits and methods related thereto. More specifically, the present invention relates to a method of diagnosing Alzheimer's Disease.

15                  Alzheimer's Disease ("AD") is the most common cause of dementia in the United States, and the presence of the disease is difficult to determine without invasive biopsies. The condition is characterized by impairments in memory, cognition, language and mobility, and these impairments progress over time.

20                  Post-mortem slices of brain tissue from AD victims show that amyloid-containing senile plaques are a prominent feature of selective areas of the AD and the Down Syndrome brain. Divry, P., *J. Neurol. Psych.*, 27: 643-657 (1927); Wisniewski, et al., "Reexamination of the pathogenesis of the senile plaque," In Zimmerman, H.M. (ed.): *Progress in Neuropathology*, N.Y. (1973), Grune and Stratton, pp. 1-26. These plaques range in size from approximately 9  $\mu\text{m}$  to 50  $\mu\text{m}$  in diameter, when viewed by immunocytochemical methods designed to detect amyloid, and they vary in morphology and density. Majocha et al., *Proc. Natl. Acad. Sci. USA*, 85: 6182-6186 (1988).  
25                  Classical staining methods can detect senile plaques as large as 200  $\mu\text{m}$ . Tomlinson, et al., "Ageing and the dementias," In: Adams, J.H., et al., (ed.), *Greenfield's Neuropathology*, Edition 4, J. Wiley and Sons, N.Y., pp. 951-1006. These plaques are most often found in the cerebral cortex, but they also occur in deeper grey matter, including the amygdaloid nucleus, the corpus striatum, and the diencephalon. Plaques have also been described in the cerebellum. Pro, et al., *Neurology*, 30: 820-825 (1980). Senile plaques are composed of

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extracellular amyloid, reactive cells, and degenerating neurites that contain Paired Helical Filaments, lysosomes, abnormal mitochondria and astrocytic processes. Wisniewski, et al., *supra* (1973). The mechanisms responsible for the excessive accumulation of amyloid, the major proteinaceous component of senile plaques, have been recently addressed at the protein chemistry, molecular biology and genetic level.

Specifically, amyloid is composed of fibrils of 4-8 nm in diameter that form the core of senile plaques. Mertz et al., *Acta Neuropathol.*, 60: 113-124 (1983). The amyloid is readily demonstrated by application of thioflavin S or Congo red to brain sections. In the latter case, polarized light causes amyloid to appear with a characteristic yellow-green color. The staining property reflects the presence of twisted beta-pleated sheet fibrils, as noted above. A detailed discussion of the biochemistry and histochemistry of amyloid can be found in Glenner, *N. Engl. J. Med.*, 302: 1333-1343 (1980).

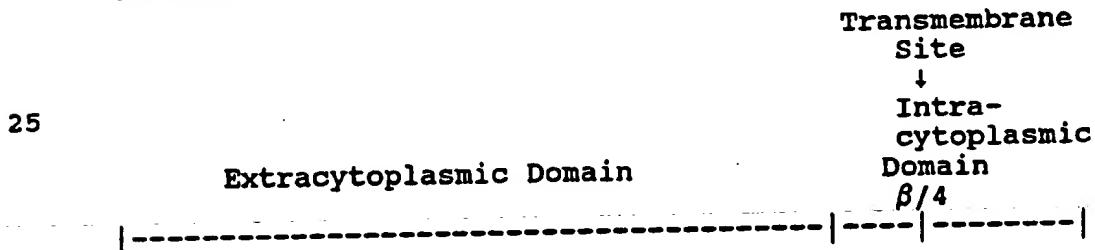
Vascular amyloidosis, referred to as congophilic angiopathy, has been recognized since the early part of this century as a significant aspect of the microscopic pathology of Alzheimer's Disease. Vinters, et al. *Stroke*, 18: 311-324 (1987). Over 90% of Alzheimer cases have congophilic angiopathy. Glenner, et al., *Ann. Pathol.*, 1: 120-129 (1981). Similar to parenchymal amyloid deposits, vascular amyloid is demonstrated by characteristic thioflavin S and Congo red staining reactions. The parieto-occipital cortex is usually more affected than that in the frontal and temporal lobes. Tomlinson et al., *supra* (1984).

In vascular amyloidosis, the amyloid appears to infiltrate the micro-vasculature, and affected vessels often pass from the leptomeninges into the cortex. Small cerebral vessels with arterioles that appear as thickened

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tubes are observed. The changes include the small pial and intracortical arterioles, the leptomeningeal vessels and the intracortical capillaries. Tomlinson et al., *supra* (1984). Immunocytochemical and electron microscopic studies have indicated that the amyloid component of senile plaques are often observed in close proximity to affected microvessels. Allsop, et al. *Neurosci. Lett.*, 68: 252-256 (1986). However, the angiopathy may occur without senile plaques. Montjoy, et al., *J. Neurol. Sci.*, 57: 89-103 (1982).

The principle component of both cerebral (senile plaques) and vascular amyloid is the 4.2 kilodalton peptide,  $\beta$ -amyloid, which is also referred to as  $\beta/A4$  and A4. Glenner et al., *Biochem. Biophys. Res. Commun.*, 120: 885 (1984).  $\beta/A4$  is derived from a parent molecule, the amyloid precursor protein (APP). Kang et al., *Nature*, 325: 733-736 (1987). At least three major variants of APP are known, having 695, 751 and 770 amino acids, respectively. In all three variants, the site of the  $\beta/A4$  peptide is in the same relative 3'-end location, as follows:



Kang et al., *supra* (1987) showed through cloning APP-695 that APP has a large extracellular domain, a transmembrane domain (which gives rise to the  $\beta/A4$  peptide) and an intracytoplasmic domain (See Figure 9). The signal sequence, for transport through the endoplasmic reticulum membrane, is followed by a region rich in cysteine, which suggests that disulfide bridges may stabilize this portion of the structure. Within the next 100 residues are a stretch of 7 uninterrupted

threonine residues and a region containing 28 glutamic acid residues and 17 aspartic residues. Marotta, et al. *J. Mol. Neurosci.*, 3: 111-125 (1992) suggest that this domain could bind cations extensively and may have physiological significance. Sodium dodecyl sulfate ("SDS") may be bound to a lesser extent than usual due to this domain. The region from residue 290 to 597, at which point the  $\beta/A4$  site begins, contains two potential N-glycosylation sites at positions 467-469 and 496-498. The  $\beta/A4$  peptide (residues 596-638 or 639) is either 42 or 43 amino acids in length and partly includes the putative transmembrane domain (amino acids 625-648). The C-terminal region of the APP is relatively small, consisting of 57 residues.

Following the transmembrane region, lysine residues are present (residues 649-651) which, according to Kang et al. *supra* (1987), could interact with phospholipid head groups in the membrane. This feature has been described for the junction between membrane and cytoplasmic domains of cell-surface receptors. One site (amino acids 684-686) is a potential glycosylation sequence.

Gandy et al. report that during in vitro studies of synthetic peptides corresponding to the cytoplasmic domain, it was observed that protein kinase C rapidly catalyzed the phosphorylation of a peptide corresponding to amino acid residues 645-661 on ser-655. Gandy et al., *Proc. Natl. Acad. Sci. USA*, 85(16): 5218-5221 (1988), suggesting that this site may be an important control region for amyloid metabolism and its interaction with other intracellular regulatory elements.

Recent research has also focused on the biological activity of  $\beta/A4$ . Specifically, it has been noted that this peptide and its fragments are trophic, toxic and/or amnestic at various concentrations. Also,  $\beta/A4$  forms insoluble aggregates (self-aggregates) under various

conditions, and the neurotoxicity of  $\beta$ /A4 is related to the aggregation process. Kirshner, et al., Proc. Natl. Acad. Sci. USA, 84: 6953-6957 (1987) and Maggio, Annu. Rev. Neurosci., 11: 13-28 (1988). Maggio et al., also 5 studied the aggregation properties of radioiodinated synthetic  $\beta$ /A4 peptides *in vitro*. Proc. Natl. Acad. Sci. USA, 89: 5462-5466 (June 1992).

Pike et al., J. Neurosci., 13(4): 1676-1687 (1993) tested the aggregation properties of an overlapping 10 series of synthetic  $\beta$ -amyloid peptides and compared them with their neurotoxic properties *in vitro*. They discovered that few peptides assembled into aggregates immediately after solubilization but that over time peptides containing the highly hydrophobic 829-35 region 15 formed stable aggregations. In short-term cultures, neurotoxicity was associated with those peptides demonstrating significant aggregations.

Thus far, diagnosis of AD has been achieved mostly through clinical criteria evaluation, brain biopsies and 20 post mortem tissue studies. However, recent work has focused on immunoassay methods for detecting markers of AD in body fluids such as spinal fluid and also in *in situ* hybridization studies using nucleic acid probes. World Patent No. 92/17152 by Potter; Warner, M., Anal. 25 Chem., 59: 1203A (1987); U.S. Patent No. 4,666,829 by Glenner et al. In U.S. application no. 105,751, the contents of which is hereby incorporated by reference, Marotta et al. describe anti- $\beta$ /A4 antibodies for purposes of *in vitro* and *in vivo* diagnostic methods.

Glenner et al., *supra*, teach the use of the  $\beta$ /A4 peptide, or fragments thereof, for the production of 30 antibodies which recognize the antigenic determinants of the polypeptide or homologues thereof.—Glenner et al. further teach the use of the disclosed polypeptide for 35 the production of nucleic acid probes which hybridize with the gene encoding the polypeptide. One such

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polypeptide has the following amino acid sequence (SEQ ID NO:1): H<sub>2</sub>N-Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-Gln-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-Lys-COOH. The diagnostic methods taught in this  
5 patent are characterized as non-invasive.

U.S. Patent Nos. 5,039,511 and 4,933,156 by Quay et al. describe the *in vitro* and *in vivo* use of iodinated imaging compounds derived from bisdiazobenzidine compounds to detect the presence and location of amyloid  
10 deposits in an organ or area of a patient.

Although  $\beta$ /A4 has been considered for use in *in vitro* diagnostic methods, this polypeptide has never been described in connection with *in vivo* diagnostic imaging methods. Therefore, a need exists for a diagnostic  
15 *in vivo* imaging method that exploits the self-aggregation properties of amyloid proteins such as  $\beta$ /A4.

Summary of the Invention

One object of the present invention is to provide an amyloid binding composition for *in vivo* imaging of amyloid deposits comprising a labeled amyloid protein which binds to amyloid deposits *in vivo* and a pharmaceutically acceptable carrier.

Another object of the present invention is to provide an *in vivo* method for detecting amyloid deposits in a subject comprising the steps of administering to a subject a detectable quantity of an amyloid binding composition comprising a labeled amyloid binding protein and a pharmaceutically acceptable carrier and detecting the binding of the labeled protein to the amyloid deposit.

Another object of the present invention is to provide a method of diagnosing an amyloidosis-associated disease, such as Alzheimer's Disease and Down Syndrome, by applying the above method to the detection of amyloid deposits in subjects suspected of having an amyloidosis-associated disease.

The amyloid binding protein of the present invention includes all variants of the amyloid protein which bind to amyloid deposits *in vivo*.

Brief Description of the Drawings

Figure 1 shows a chart setting forth chemically documented amyloidosis with protein types.

Figure 2 depicts a PAGE-SDS gel of the A4-O synthetic amyloid peptide. The amyloid polypeptide of 28 residues, corresponding to the previously reported sequence of Masters et al., Proc. Natl. Acad. Sci. USA 82: 4245-4249 (1985) was synthesized on a Biosearch SAM2 synthesizer using the general procedure of Merrifield, J. Am. Chem. Soc., 85: 2149-2154 (1963). Purification was achieved with a 3 X 65 cm column of Sephadex G50 (10-40  $\mu$ ). The peptide (10  $\mu$ g) was suspended in sample buffer containing 2% SDS (Brown, et al., J. Neurochem., 40: 299-308 (1983))

and 9.5 M urea. Electrophoresis was carried out on a uniform 10% gel containing 0.1% SDS. (A) Molecular weight markers: phosphorylase B (94 kd), bovine serum albumin (68 kd), ovalbumin (43 kd), carbonic anhydrase (29 kd), trypsin inhibitor (22 kd), lysozyme (14.5 kd). (B) The synthetic amyloid peptide ran as a sharp band at the front of the gel and as an aggregated form of higher molecular weight.

Figure 3 depicts gel electrophoresis of the synthetic peptides A4-O and P2 (APP amino acids 413-429). (Panel a): Twenty ug of A4-O (lane 1) and P2 (APP amino acids 413-429) (lane 2) were analyzed by 18% SDS-PAGE (acrylamide : bisacrylamide = 30 : 0.8). (Panel b): Analysis of A4-O and P2 (APP amino acids 413-429) on 11% SDS/urea-PAGE (acrylamide : bisacrylamide = 20 : 1). Lanes 1-3 containing A4-O (10 ug) were incubated with 2% SDS and 5% 2-ME at 95°C for 5 minutes (Lane 1), 30 min (Lane 2) and 60 minutes (Lane 3). Lane 4 contained P2 (10ug). Gels were stained with Coomassie Brilliant blue R-250. Molecular weights are shown on the right (Kd).

Figure 4 shows slot blots of immunostained A4-O after addition of itself or a second A4 homologue. This assay depicts the increase staining intensity after A4 homologues are added to one another. This reflects the ability of homologues to self-aggregate and thus increase the staining intensity. In each case, the slot contained 1 ug of A4 peptide. To each, 2.5, or 10.0 ug of exogenous peptide was added, as indicated. The blots were then immunostained (see descriptions of Figures 5, 6 and 7).

Figure 5 shows immunoblots with and without exogenous A4-O peptide. Density values of the immunoreaction products of A4-O with and without exogenous peptides after reaction with 10H3. The values of the bars correspond to the density of blots shown in Figure 4. The description of Figure 4 indicates the condition of

each blot with regard to the exogenous peptide that was added to the blotted peptide prior to addition of 10H3. The height of the bars above the black bar (no peptide addition) is a measure of the extent to which the exogenous peptide bound to the attached peptide on the filter paper and increased the density of immunostaining of the complex.

At the three indicated concentrations (2.5, 5.0 and 10.0 ug/ml) A4-O was added to the A4-O that was already present at a concentration of 1 ug. The blot was then immunostained to develop the colored reaction product. The data were derived from scanning Figure 4.

Figure 6 shows immunoblots with and without exogenous A4-H peptide. At the three indicated concentrations (2.5, 5.0 and 10.0 ug/ml) A4-H was added to the A4-O that was already present at a concentration of 1 ug. The blot was then immunostained to develop the colored reaction product. The data were derived from scanning Figure 4. See description of Figure 5 for more details.

Figure 7 shows immunoblots with and without exogenous Op1 peptide. At the three indicated concentrations (2.5, 5.0 and 10.0 ug/ml) Op1 was added to the A4-O that was already present at a concentration of 1 ug. The blot was then immunostained to develop the colored reaction product. The data were derived from scanning Figure 4. See description of Figure 5 for more details.

Figure 8 shows the reactivity of 10H3 towards A4-O (upper panel).

Figure 9 (SEQ ID NOS:11 and 12) is the nucleotide sequence and predicted amino acid sequence of cDNA encoding the precursor protein (APP) of the  $\beta$ /A4 with the  $\beta$ /A4 region boxed, as set forth in Kang et al., *supra*, (1987).

Detailed Description of the Preferred Embodiments

Applicants have discovered that an amyloid binding composition comprising a labeled amyloid protein may be used *in vivo* for detecting the presence and 5 location of amyloid deposits. The amyloid binding composition of the present invention comprises a labeled amyloid protein and a pharmaceutically acceptable carrier. This protein is any natural or synthetic protein which binds to amyloid deposits *in vivo*. In one 10 embodiment, the protein is the  $\beta$ -amyloid polypeptide ( $\beta$ /A4 peptide), which in its longest form has 42 to 43 amino acid residues, as shown in Figure 9. See Masters, et al., *Proc. Nat. Acad. Sci., USA.*, 82: 4245-4249 (1985).

As noted above,  $\beta$ /A4 is derived from a larger amyloid precursor protein having from 695 to 770 amino acids. See 15 Kang et al., *Nature*, 325: 733 (1987). The term "amyloid deposit" includes amorphous, eosinophilic materials that are associated with amyloidosis, a disease complex 20 including over 20 different clinically defined syndromes, as discussed above. Chemically, amyloid deposits are proteinaceous, and their chemical compositions are unique 25 for each of the clinical syndromes with which they are associated, as set forth in Figure 1. Preferably, the amyloid deposit of the present invention is that found in the brain of Alzheimer's Disease patients. As noted above, such amyloid deposits are found in senile plaques 30 in selected areas of the AD brain and are composed of fibrils of 4-8 nm diameter. These plaques are detected by application of thioflavin S or Congo red to brain sections and in the latter case, appear yellow-green under polarized light. They have twisted beta-pleated sheet fibrils and are further characterized by Glenner, 35 *N. Eng. J. Med.*, 302: 1333-1343 (1980). In another embodiment, the amyloid deposit of the present invention is that which is associated with vascular amyloidosis, as

described in Vinters, *Stroke*, 18: 311-324 (1987).  
vascular amyloid deposits infiltrate the cerebral micro-  
vasculature. Similar to amyloid deposits found in  
senile plaques in the parenchyma of the AD brain,  
5 vascular amyloid deposits have characteristic thioflavin  
S and Congo red staining reactions. Montjoy et al., *J.  
Neurol. Sci.*, 57: 89-103 (1988).

The term "amyloidosis-associated disease" includes  
any disease characterized by local or systemic amyloid  
10 deposits. (See Figure 1) Preferably, the amyloidosis-  
associated disease of the present invention is  
Alzheimer's Disease or Down Syndrome.

In addition to amyloid protein purified from natural  
sources such as cerebrovascular tissue, as described  
15 hereinafter, amyloid protein of the present invention  
includes recombinant and synthetic amyloid protein and  
variants of the naturally occurring, recombinant and  
synthetic protein. In a preferred embodiment, the  
20 amyloid protein of the invention comprises the  $\beta$ -amyloid  
polypeptide and variants thereof. The category of  
"variants" includes, for example, a fragment of the  $\beta$ -  
amyloid polypeptide or any homologous amino acid sequence  
or amino acid addition, wherein the resulting polypeptide  
25 has the same or similar function as the natural occurring  
polypeptide in that it binds to amyloid deposits *in vivo*.  
In one embodiment, the amyloid protein of the present  
invention is comprised of the  $\beta$ -amyloid polypeptide or  
variant thereof and amino acids from the APP protein  
30 which are from regions of the APP protein which are  
either adjacent or non-adjacent to the  $\beta$ -amyloid  
polypeptide. For example, in one embodiment, the amyloid  
protein of the present invention comprises:

(A) — The  $\beta$ /A4-peptide alone (SEQ ID NO:2):  
Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-Glu-Val-His-His-  
35 Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-Lys-

Gly-Ala-Ile-Ile-Gly-Leu-Met-Val-Gly-Gly-Val-Val-Ile-Ala-Thr; or

- (B) The  $\beta$ /A4 peptide plus the amino acids of the transmembrane domain of the APP (SEQ ID NO:3):
- 5 Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-Glu-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met-Val-Gly-Gly-Val-Val-Ile-Ala-Thr-Val-Ile-Val-Ile-Thr-Leu-Val-Met-Leu; or
- 10 (C) The  $\beta$ /A4 peptide plus the remaining C-terminal amino acids of the entire APP (SEQ ID NO:4):
- Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-Glu-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met-Val-Gly-Gly-Val-Val-Ile-Ala-Thr-Val-Ile-Val-Ile-Thr-Leu-Val-Met-Leu-Lys-Lys-Gln-15 Tyr-Thr-Ser-Ile-His-His-Gly-Val-Val-Glu-Val-Asp-Ala-Ala-Val-Thr-Pro-Glu-Glu-Arg-His-Leu-Ser-Lys-Met-Gln-Gln-Asn-Gly-Tyr-Glu-Asn-Pro-Thr-Tyr-Lys-Phe-Phe-Glu-Gln-Met-Gln-Asn; or
- 20 (D) The  $\beta$ /A4 peptide with the preceding 10 amino acids of the APP (SEQ ID NO:5):
- Lys-Thr-Glu-Glu-Ile-Ser-Glu-Val-Lys-Met-Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-Glu-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met-Val-Gly-Gly-Val-Val-Ile-Ala-Thr; or
- 25 (E) The  $\beta$ /A4 peptide with any other APP amino acids attached to it that are not normally adjacent (SEQ ID NO:6):
- X-Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-Glu-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met-Val-Gly-Gly-Val-Val-Ile-Ala-Thr-Y,
- 30 wherein X and Y are one or more APP amino acids which are not adjacent to  $\beta$ /A4 in the nature; and
- (F) any fragment of (A)-(E), wherein said fragment is large enough to bind amyloid deposit in vivo.

The term "fragment" includes a linear amino acid subsequence of the  $\beta$ -amyloid polypeptide, wherein such fragment binds amyloid deposits *in vivo*. A variant which contains an amino acid sequence variation or substitution 5 is a homologous sequence. "Homology" between two sequences connotes a likeness short of identity indicative of a derivation of the first sequence from the second. For example, a polypeptide is "homologous" to  $\beta$ -amyloid polypeptide if it contains an amino acid sequence 10 similar enough to the natural sequence so as to confer the same or similar amyloid binding property as the natural  $\beta$ -amyloid polypeptide. Such a sequence may be only a few amino acids long and may be a single linear sequence or one or more linear sequences which confer 15 binding activity to the polypeptide when amino acids from separated portions of a linear sequence are spatially juxtaposed after protein folding. The variants encompassed by this invention can be ascertained, for example, by the *in vitro* quantitative assays described 20 below in Examples 3-7. That is, applicants have conducted a series of studies involving the addition of increasing concentrations of  $\beta$ -amyloid polypeptide variants to a solid support containing a specific peptide called A4-0. The increase in density of immunostain 25 using an anti-A4-0 monoclonal antibody, 10H3, described in U.S. Patent application no. 105,751 by Marotta, et al., incorporated by reference above, was measured. Based upon this work, it was possible to determine which peptides were suitable for use in the *in vivo* methods, 30 according to the invention. Other poly- and/or monoclonal antibodies suitable for this assay can be produced by methods well known in the art. See Kennett et al., *Monoclonal Antibodies-Hybridomas: A New Dimension in Biological Analysis*, Plenum Press (1980) 35 Protein which qualifies as "amyloid protein" according to the above criteria can be produced by

methods known and emerging in the art, including conventional reverse genetic techniques, i.e., by designing a genetic sequence based upon an amino acid sequence or by conventional genetic splicing techniques.

5 For example,  $\beta$ -amyloid polypeptide variants can be produced by techniques which involve site-directed mutagenesis or oligonucleotide-directed mutagenesis. See, for example, "Mutagenesis of Cloned DNA," in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY 8.0.3 et seq. (Ausubel, et al. eds. 1989) ("Ausubel").

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Other amyloid protein variants within the present invention are molecules that correspond to a portion of the  $\beta$ -amyloid polypeptide, but are not coincident with the natural molecule, and display the binding activity of the natural molecule when presented alone or, alternatively, when linked to a carrier or biologically active signal sequence that permits proteins to pass through membranes. See von Heijne, G., J. Mol. Biol., 184: 99-105 (1985). An amyloid protein variant of this type could represent an actual fragment, as discussed above, or could be a polypeptide synthesized *de novo* or recombinantly.

To be used in recombinant expression of amyloid protein or amyloid protein variant, a polynucleotide molecule encoding such a molecule would preferably comprise a nucleotide sequence, corresponding to the desired amino acid sequence, that is optimized for the host of choice in terms of codon usage, initiation of translation, and expression of commercially useful amounts of, for instance,  $\beta$ -amyloid polypeptide or  $\beta$ -amyloid polypeptide variant. Also, the vector selected for transforming the chosen host organism with such a polynucleotide molecule should allow for efficient maintenance and transcription of the sequence encoding the polypeptide. The encoding polynucleotide molecule may code for a chimeric protein; that is, it can have a

nucleotide sequence encoding a biologically active part of the  $\beta$ -amyloid molecule operably linked to a coding sequence for a non- $\beta$ -amyloid moiety, such as a signal peptide for the host cell.

5       For instance, in order to isolate a DNA segment which encodes a  $\beta$ -amyloid molecule, total DNA from cerebrovascular tissue can be prepared according to published methods. See, for example, Maniatis, et al., MOLECULAR CLONING: A LABORATORY MANUAL (Cold Spring  
10      Harbor Laboratories, NY 1982); Baess, *Acta Pathol. Microbiol. Scand. (Sect. B)*, 82: 78084 (1974). The DNA thus obtained can be partially digested with a restriction enzyme to provide an assortment of genomic fragments. An enzyme with a tetranucleotide recognition  
15      site, such as Sau3A (*MboI*), is suitable for this purpose. The fragments from such a partial digestion then can be size-fractionated, for example, by sucrose gradient centrifugation (see Maniatis, *supra*) or by pulsed field gel electrophoresis (See Anad, *Trends in Genetics*,  
20      November 1986, at pages 278-83), to provide fragments of a length commensurate with that of DNA encoding the  $\beta$ -amyloid molecule. Molecular cloning of amyloid cDNA derived from mRNA of the Alzheimer brain and the expression thereof is described in detail in Zain et al.,  
25      *Proc. Natl. Acad. Sci. USA.*, 85: 929-933 (1988) and Marotta et al., *Proc. Natl. Acad. Sci. USA.*, 86: 337-341 (1989), respectively, both of which are herein incorporated by reference.

According to well-known methods described, for  
30      example, in Ausubel at 5.0.1 et seq., the selected fragments can be cloned into a suitable cloning vector. A DNA sequence thus obtained could be inserted, for example, at the *BamH1* site of the *pUC18* cloning vector which is transfected into appropriate host cells such as *E. coli* or a mammalian cell. A variety of screening  
35

mechanisms known in the art of the invention can then be used to identify clones containing the  $\beta$ -amyloid gene.

In another embodiment of the invention, amyloid protein of the present invention is purified from tissue samples. For example, brains from Alzheimer's Disease post-mortum patients are histologically sectioned and stained with Congo Red dye. Upon visualization with a polarizing microscope, amyloid deposits can be identified by their green color. Brains exhibiting extensive cerebrovascular amyloidosis are used as source for purified amyloid protein. After removal of contaminants from the amyloid containing vessels of the meninges, the meningeal tissues are homogenized and centrifuged to yield a brownish layer rich in amyloid fibrils. This layer is then digested with collagenase, solubilized in 6M guanidine HCl, pH 8.0 and centrifuged. The supernatant containing the solubilized protein is desalted by dialysis and gel exclusion column chromatography and high performance liquid chromatography is used to purify the polypeptide. The amino acids for the purified protein (e.g.,  $\beta$ -amyloid polypeptide) are then sequentially cleaved in an automated amino acid sequencer, such as a Beckman 890 C spinning cup sequencer, and analyzed by high performance liquid chromatography in order to determine the amino acid sequence of the amyloid protein. See Glenner & Wong, *Biochem. Biophys. Chem. Res. Commun.*, 120: 885 (1984).

In another embodiment, amyloid protein and variants thereof can be produced in accordance with published methods. For instance, Kirschner et al., *Proc. Natl. Acad. Sci. USA*, 84: 6953-57 (1987) used an ABI Synthesizer model 380 B (Applied Biosystems, Foster City, CA) to synthesize synthetic  $\beta$ -amyloid peptides consisting of residues 1-28 and homologues thereof. General methods for peptide synthesis can be found in Clark Lewis et al., *Science*, 231: 134 (1986). See also, Hilbich et al., *J.*

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Mol. Biol., 218: 149-163 (1991); Majocha et al., Proc. Natl. Acad. Sci. USA, 85: 6182-6186 (1988); and U.S. Patent application No. 105,751 by Marotta et al.

5       The term "in vivo imaging" refers to any method that permits the detection of a labeled amyloid protein which binds to amyloid deposits located in a subject's body. A "subject" is a mammal, preferably a human. Often, particularly when the composition and method of the invention is directed to the diagnosis of Alzheimer's 10 Disease or Down Syndrome, the subject will manifest clinical symptoms of the suspected amyloidosis. These clinical symptoms are well-known to the practitioner of this invention and include loss of memory, and other impairments described above.

15      The amyloid binding composition of the present invention must be of a "detectable quantity." A detectable quantity is that which is sufficient to enable detection of the site of amyloid deposit location when compared to a background signal. The dosage of the 20 amyloid binding composition will vary depending upon such considerations as age, condition, sex, extent of disease in the patient, counterindications, and other variables, to be adjusted by the individual physician. Dosage can vary from

25      0.01 mg/kg to 2,0000 mg/kg, preferably 0.1 mg/kg to 1,000 mg/kg.

In accordance with this invention, the amyloid protein may be labeled by any of several techniques known to the art. See, e.g., Wagner et al., J. Nucl. Med., 20: 30 428 (1979); Sundberg et al., J. Med. Chem., 17: 1340 (1974) and Saha et al., J. Nucl. Med., 6: 542 (1976).

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35      The label is chosen based upon the type of detection instrument employed. For instance, a chosen radionucleotide must have a type of decay which is detectable for a given type of instrument. An ther

consideration relates to the half-life of the isotop . The half-life should be long enough so that it is still detectable at the time of maximum uptake by the target, but short enough so that the host does not sustain deleterious radiation. Preferably, the chosen label will lack a particulate emission, but will produce a large number of photons in a 140-200 keV range, which may be readily detected by, for instance, conventional gamma camera. Suitable radioisotopes for purposes of this invention include, gamma-emitters, position-emitters, x-ray emitters and fluorescence-emitters. These radioisotopes include Iodine-131, Iodine-123, Iodine-126, Iodine-133, Bromine- 77, Indium-111, Indium-113m, Gallium-67, Gallium-68, Ruthenium-95, Rutheium-97, Ruthenium-103, Ruthenium-105, Mercury-107, Mercury-203, Rhenium-99m, Rhenium-105, Rhenium 101, Tellurium-121m, Tellurium-122m, Tellurium-125m, Thulium-165, Thulium-167, Thulium-168, Technetium-99m and Fluorine-18. The preferred radiolabel is Technetium-99m. Suitable paramagnetic isotopes for use in Magnetic Resonance Imaging (MRI), according to this invention, include <sup>157</sup>Gd, <sup>55</sup>Mn, <sup>162</sup>Dy, <sup>59</sup>Cr, and <sup>56</sup>Fe.

Administration to the subject may be accomplished intraventricularly, intravenously, intraarterially, via the spinal fluid or the like. Administration may also be intradermal or intracavitory, depending upon the body site under examination. After a sufficient time has lapsed for the labeled amyloid protein to bind with amyloid deposits, for example 30 minutes to 48 hours, the area of the subject under diagnosis is examined by routine imaging techniques such as MRI, SPECT and planar scintillation imaging. The exact protocol will necessarily vary depending upon factors specific to the patient, as noted above, and depending upon the body site under examination, method of administration and typ f label used; the determination of specific procedur s

would be routine to the skilled artisan. The distribution of the bound radioactive isotope and its decrease with time is then monitored and recorded. By comparing the results with data obtained from studies of 5 clinically normal individuals, the presence and location of amyloid deposits can be determined.

Thus, in one embodiment, the methods of the present invention is used to diagnoses an amyloidosis-associated disease. Where the site of examination is the brain, the 10 *in vivo* detection of amyloid deposits according to the methods of the present invention signifies a diagnosis of Alzheimer's Disease. The detection of amyloid deposits in the brain of patients manifesting clinical symptoms of Down Syndrome, signifies a diagnosis of Down Syndrome. 15 In that regard, applicants note that the gene for APP, located on chromosome 21, is over-represented in Down Syndrome individuals (Serra et al., Amer. J. Med. Gen. Supp., 7: 11-19 (1990)). Accumulations of amyloid occur in young Down Syndrome patients, with nearly 90% of Down Syndrome subjects aged less than 30 years showing amyloid 20 accumulation (Hyman, Prog. Clin. Biol. Res. 379: 123-142 (1992)). The Down Syndrome patient displays amyloid accumulations early in life, often by late teenage years. As adults, nearly 100% will develop Alzheimer Disease 25 (Cork, Amer. J. Med. Gen. Supp., 7: 282-539 (1990)). The neuropathology of Down Syndrome is essentially identical to that of Alzheimer Disease and includes  $\beta$ /A4 amyloid deposits in senile plaques. The Alzheimer - like lesions represent a major neuropathologic trait of the brain of 30 the Down Syndrome patient (Serra et al., Supra (1990)).

The amyloid-binding compositions of the present invention are advantageously administered in the form of injectable compositions. A typical composition for such purpose comprises a pharmaceutically acceptable carrier. 35 For instance, the composition may contain about 10 mg of

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human serum albumin and from about 20 to 200 micrograms of the labeled amyloid prot in per milliliter of phosphate buffer containing NaCl. Other pharmaceutically acceptable carriers include aqueous solutions, non-toxic excipients, including salts, preservatives, buffers and the like, as described in REMINGTON'S PHARMACEUTICAL SCIENCES, 15th Ed. Easton: Mack Publishing Co. pp 1405-1412 and 1461-1487 (1975) and THE NATIONAL FORMULARY XIV., 14th Ed. Washington: American Pharmaceutical Association (1975), the contents of which are hereby incorporated by reference. Examples of non-aqueous solvents are propylene glycol, polyethylene glycol, vegetable oil and injectable organic esters such as ethyloleate. Aqueous carriers include water, alcoholic/aqueous solutions, saline solutions, parenteral vehicles such as sodium chloride, Ringer's dextrose, etc. Intravenous vehicles include fluid and nutrient replenishers. Preservatives include antimicrobials, anti-oxidants, chelating agents and inert gases. The pH and exact concentration of the various components of the binding composition are adjusted according to routine skills in the art. See GOODMAN AND GILMAN'S THE PHARMACOLOGICAL BASIS FOR THERAPEUTICS (7th ed.). The skilled artisan would also readily appreciate that a suitable excipient or carrier would need to prevent aggregation of the binding composition prior to contacting the target amyloid deposit in vivo.

Particularly preferred amyloid binding compositions of the present invention are those that, in addition to binding to amyloid deposits in in vivo, are also non-toxic at appropriate dosage levels, have a satisfactory duration of effect, and display an adequate ability to cross the blood-brain barrier. In this regard, United States Patent No. 4,540,564 discloses an approach for enhancing blood-brain barrier-penetrating ability by attaching a centrally acting drug species to a reduced,

biooxidizable, lipoidal form of dihydropyridine pyridinium salt redox carrier. Thus, in one embodiment, the composition of the present invention includes such a blood-brain barrier crossing enhancer carrier.

5       In vivo animal testing provides yet a further basis for determining dosage ranges, efficacy of transfer through the blood barrier and binding ability. Particularly preferred for this purpose is the "senile animal" model for cerebral amyloidosis -- animals such as  
10      aged dogs or monkeys, which are known to develop variable numbers of Alzheimer-type cerebral senile plaques, see Wisniewski, -et-al., J. Neuropathol. & Exp. Neurol., 32: 566 (1973), Selkoe, et al., Science, 235: 873 (1987) are tested for binding and detection efficacy. This in vivo  
15      assay requires control-biopsy monitoring to confirm and quantify the presence of amyloid deposits.

Also, cellular models of amyloidosis have been prepared that overproduce  $\beta$ -amyloid polypeptide in animals for purposes of testing the efficacy of the amyloid binding compositions and methods of the present invention. See Marotta, et al. Proc. Natl. Acad. Sci. USA, 86: 337-341 (1989). Such cell models have been adapted to a behavior paradigm. See Tate-Ostroff, Proc. Natl. Acad. Sci. USA 89: 7090-7094, (1992). That is,  
25      because AD patients suffer circadian rhythm dysfunction, this behavioral deficit was modeled in rats by a cell grafting techniques. PC12 cells transfected with the  $\beta$ -amyloid polypeptide C-terminal region of the APP were implanted into the suprachiasmatic nuclei ("SCN") of rats; the SCN is a primary circadian oscillator in mammals. Animals receiving amyloidotic cell grafts, but not animals receiving control cell grafts, exhibited  
30      disrupted activity rhythms, although temperature rhythms were unaffected. The specificity of the disruption was similar to circadian dysfunction seen in AD patients.  
35      The data supported an association between a defined

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behavioral disruption and amyloid overexpression either directly or through the release of cellular factors as a consequence of amyloid overproduction.

Other suitable animal models for use in testing the compositions and methods of the present invention are produced transgenically. For instance, Quon et al., *Nature*, 352: 239-241 (1991) used rat neural-specific enolase promoter inhibitor domain to prepare transgenic mice. See also, Wirak et al., *Science*, 253: 323-325 (1991). Still other models have been produced by intracranial administration of the  $\beta$ /A4 peptide directly to animals-(Tate et al., *Bull. Clin. Neurosci.*, 56: 131-139 (1991)).

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The following examples are merely illustrative and not limitative of the remainder of the disclosure in any way whatsoever.

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#### EXAMPLES

As noted above, A4 is intended to be the same as  $\beta$ /A4, throughout the examples. The peptides used in the following Examples have the following structures:

5      A4-O (peptides 1-28), SEQ ID NO:7:

N-Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-Glu-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Ser-Ala-COOH

10     The A4-O(1-28) polypeptide that was reported in Masters, et al. Proc. Nat'l. Acad. Sci. U.S.A., 82: 4245-4249 (1985) is the first 28 amino acids of the 4.2 Kd peptide derived from senile plaque cores of an AD brain. Masters, et al. have also shown that the naturally occurring peptide aggregates even in denaturing gels.

15     The A4-O(1-28) sequence of this invention was synthesized by Biosearch in San Rafael, CA. The underlined amino acids differ from A4-P(1-28), as shown below.

A4-H (peptides 1-28):

20     The A4-H peptide is the same as A4-O(1-28) except that it was synthesized by the Harvard Microchemistry Laboratory.

A4-P (peptides 1-28), SEQ ID NO:8:

N-Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-Gln-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-Lys-COOH

25     This sequence was reported by Glenner and Wong, supra, (1984) and derived from vascular amyloid of the AD brain and from a Down Syndrome brain. Three of 28 amino acids are different from the A4-O/A4-H peptides (underlined).

A4-B (peptides 1-28), SEQ ID NO:9:

N-Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-Glu-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-Lys-COOH

30     This sequence was obtained from Bachem and is the 28 amino acid structure that is commonly determined from

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molecular cloning studies (Kang, et al., *Nature (London)* 325: 733-736 (1987)). Unlike the Glenner and Wong, supra, sequence (A4-P(1-28)), it has Glu, not Gln, at position 11. And, unlike A4-O/A4-H, it has Asn-Lys and not Ser-Ala at the C-terminus.

5 Op1 (peptides 1-10), SEQ ID NO:10:

N-Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-COOH

10 A4(1-10) consists of the first 10 amino acids of the amyloid peptide derived from any source and is described in U.S. Patent No. 4,666,829 by Glenner et al. Thus far, this sequence appears conserved in all reports on amyloid that is derived from non-Familial AD cases. The A4-(1-10) antigen used in the present studies was synthesized by the Harvard Microchemistry Laboratory.

15 Summary of sequence variations: dashed line indicates sequence conservation among the peptides shown.

A4-O (1-28): N-----	Glu-----	Ser-Ala-	(Masters)
A4-H (1-28): N-----	Glu-----	Ser-Ala-	(Masters)
A4-P (1-28): N-----	Gln-----	Asn-Lys-	(Glenner)
20 A4-B (1-28): N-----	Glu-----	Asn-Lys-	(Kang)
Op1 : N-----			

Example 1. Self-aggregation of the A4-O amyloid peptide  
in SDS/urea acrylamide gels

The synthetic  $\beta$ -amyloid 28-mer polypeptide, A4-O (Masters, et al., *supra*) was analyzed by polyacrylamide gel electrophoresis (PAGE) procedures (Brown, et al., *J. Neurochem.*, 40: 299-308 (1983)) and was noted to have unusual aggregation properties. The peptide was dissolved in a PAGE sample buffer containing SDS and urea and was electrophoresed on a 10% gel containing SDS (See description of Figure 2). After staining with Coomassie blue, the peptide appeared as a broad band at approximately 23-25 kd and a narrow band that migrated at the gel front during electrophoresis (See Figure 2). The higher molecular weight species appeared to be an aggregate since it was eliminated by adding urea to the separating gel and, subsequently, a 3-4 kd band was obtained (not shown). Polyclonal antiserum to the 28-mer was prepared and applied to nitrocellulose blots of an overloaded gel. The latter contained a series of aggregated peptides of various apparent molecular weights, all of which reacted with the antiserum. Thus, the synthetic 28-mer had aggregational properties not unlike the naturally occurring A4-O amyloid protein of 4 kd (Masters, et al., *supra*).

Applicants' studies demonstrating the aggregation properties of the A4-O peptide were previously reported (Salim, et al., "Molecular Cloning of Amyloid cDNA from Alzheimer Brain Messenger RNA" in *Familial Alzheimer's Disease*, J.P. Blass et al. eds., Marcel Dekker, NY pp 153-165 (1988)).

Based upon the results shown in Figure 2, applicants concluded that even in the presence of strong denaturing agents and after electrophoresis, A4-O strongly bound to itself.

Example 2: Self-aggregation of A4-O peptid on highly cross-linked SDS/urea acrylamide gels

Applicants obtained confirmatory data using the highly cross-linked acrylamide gel system described by  
5 Honda and Marotta, Neurochem. Res., 17: 367-374 (1992).

When analyzed by this gel system containing SDS and urea, the synthetic peptide A4-O migrated as a broad series of bands below an apparent molecular weight of 15kDa (data not shown). However, when 6M urea was added  
10 to the PAGE system the peptide appeared as a sharp single band of 15kDa (Figure 3) and smaller size bands were not observed even after silver staining (data not shown). By contrast, peptide P2(413-429), used as a control and corresponding to an extracytoplasmic region of the  $\beta$ /A4  
15 precursor protein, migrated with the bromphenol blue dye front on both SDS-PAGE and SDS/urea-PAGE systems (Figure 3, lane 4). Since the theoretical molecular weight of the 28 amino acid peptide A4-O is 3,178 Da the results indicate that the band of 15kDa is an aggregate.  
20 Migration of A4-O peptide bands on both gel systems was not affected by 2-ME nor by pre-treatment with 80% formic acid (data not shown).

The 15kDa was visible after peptide A4-O were treated for 5 minutes at 95°C prior to electrophoresis (Figure 3, lane 1). When boiling time was increased to 30 minutes or 60 minutes the aggregate partly dissociated to a smaller size (Figure 3, lanes 2 and 3). This dissociation was not dependent on the presence of SDS and 2-ME in the sample buffer but rather on the time of heat  
25 denaturation. These data were previously reported (Honda and Marotta, *supra*).

Applicants concluded that Figure 3 confirms that even in the presence of strong denaturing agents and heat treatment after electrophoresis, A4-O strongly bound to  
35 itself.

Example 3: Self-aggregation of A4 peptides on immunoblots

Due to the desirability of obtaining a quantitative assay for the selection of  $\beta$ -amyloid polypeptides for the composition and methods of the present invention, applicants elected to use quantitative slot blots to test aggregation of peptides rather than tissue slices. The general immunoblotting procedure utilizing A4 peptides attached to a solid support and detectable by applied anti-amyloid antibodies was reported earlier (Majocha, et al., *supra*, (1988)). In all cases, the monoclonal antibody used to detect A4 aggregates was 10H3 (2 ug/ml).

One microgram of each of the indicated peptides were added overnight at room temperature to Millipore P filter paper to which A4-O was attached. The peptides were dissolved in ICC buffer: 2% BSA, 0.3M NaCl, 20mM Tris, 0.01% Triton. The blots were immunoprocessed (Majocha, et al. *supra*) and then optically scanned for density; the areas under the curves were integrated by means of an LKB Laser Densitometer.

Peptides A4-O, A4-H and Opi were applied to filters to which was bound peptide A4-O, the antigen used to prepare mab 10H3. The experiment was designed to test the competence of each of the applied peptides to bind to the bound peptide. While A4-O and A4-H have the same primary structure, it has been noted that peptides with identical sequences that are obtained from different sources may have non-identical properties. (See Figure 4).

The density of staining (the optical density of the immunoreaction product) is quantitated in Figures 5, 6 and 7. The OD is a measure of the extent of the aggregation since it will be related to the antibody concentration and thus the color reaction.

The density values shown in Figure 5 were obtained by densitometric scanning of the reaction product on

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blots from which the control value (no primary antibody) was subtracted. A further control was one in which the mab 10H3 was added to blots containing Opl in the absence of added exogenous peptide. This control value 5 represents the antibody-antigen reaction without interference from added peptides.

Based upon the results presented in Figure 5, applicants concluded that A4-O bound to itself with at an optimal concentration of 5.0 ug/ml.

10 Example 4: Self-aggregation of A4-H peptides on immunoblots

The experiment of Example 3 was repeated except that the exogenous peptide was A4-H. The data are shown in Figure 6 and based upon these results, applicants 15 concluded that A4-H bound to A4-O at an optimal concentration of 2.5 ug/ml.

Example 5: Self-aggregation of Op1 peptides on immunoblots

5 The experiment of Example 3 was repeated except that the exogenous peptide was Op1. The data are shown in Figure 7 and based upon these results, applicants concluded that Op1 bound to A4-O at an optimal concentration of 2.5 ug/ml.

10 Based upon the results presented in Figures 5, 6 and 7, applicants concluded that three peptides bound the filter-bound A4-O peptide and increased the extent to which 10H3 reacted. The reaction is concentration-dependent. The three peptides, A4-O, A4-H and Op1, aggregated to the attached A4-O. The Op1 10-mer reacted nearly as well or better, at 2.5 ug, as the larger 28-  
15 mers.

Example 6: Specificity of 10H3 for both A4-O and Op1

The results shown in Figure 7 indicate that a small peptide, a ten-mer, was able to bind at least as well as 1-28-mers to an A4 substrate.

20 Thus, this assay, which measures the optical density of the reaction product between the added 10H3 mab and the Op1 peptide on the solid surface, reflected the presence of the exogenous peptide, as applicants previously demonstrated for the reaction between 10H3 and  
25 A4-O.

With respect to Op1, additional studies were carried out to confirm the reactivity of 10H3. On separate solid supports (Millipore P paper) either the A4-O antigen (2ug/slot) or the Op1 antigen (2 ug/slot) were absorbed  
30 using a slot blot apparatus. The results are shown in Figure 8, as follows:

Reactivity of 10H3 towards A4-O (upper panel):

Blot no.:

- 35 1. Immunostain lacking the primary antibody (10H3) show d no reactivity with the blot, as expect d.

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2. 10H3 was very strongly reactive with its own antigen, A4-O.
  3. Soluble A4-O antigen added to the mix caused inhibition of 10H3 towards A4-O.
  - 5 4. Soluble Opi added to the mix caused inhibition of 10H3 towards A4-O.
  5. 10H3 was reactive towards the Opi antigen.
  6. Soluble Opi added to the mix showed inhibition of 10H3 towards Opi.
- 10 The slot blots were quantified by densitometry and numerical values were obtained that indicated the extent of the reaction between 10H3 and antigens. These values are given below in Table I in which each numbered item refers to the blot number in Figure 8 and the description  
15 given above:

---

Table I: Optical Density of Reaction Between 10H3 and Either A4-O or Opi Antigens in Blots of Figure 7

---

Slot Number:	1	2	3	4	5	6
OD Units:	0.03	0.70	0.31	0.18	0.16	0.07

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Based upon the results presented in Figure 8 and Table I, applicants concluded that 10H3 is reactive with its own A4-O antigen as well as with the Opi peptide.

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: THE MIRIAM HOSPITAL
- (ii) TITLE OF INVENTION: Composition and Method for in Vivo Imaging of Amyloid Deposits
- (iii) NUMBER OF SEQUENCES: 13
- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Foley & Lardner
  - (B) STREET: 3000 K Street, N.W., Suite 500
  - (C) CITY: Washington, D.C.
  - (E) COUNTRY: USA
  - (F) ZIP: 20007-5109
- (v) COMPUTER READABLE FORM:
  - (A) MEDIUM TYPE: Floppy disk
  - (B) COMPUTER: IBM PC compatible
  - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
  - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 27 May 1994
  - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
  - (A) NAME: SAXE, Bernhard D.
  - (B) REGISTRATION NUMBER: 28,665
  - (C) REFERENCE/DOCKET NUMBER: 57548/103/MIHO
- (ix) TELECOMMUNICATION INFORMATION:
  - (A) TELEPHONE: (202)672-5300
  - (B) TELEFAX: (202)672-5399
  - (C) TELEX: 904136

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 28 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Gln Val His His Gln Lys  
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 43 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys  
1 5 10 15  
Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile  
20 25 30  
Gly Leu Met Val Gly Gly Val Val Ile Ala Thr  
35 40

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 52 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys  
1 5 10 15  
Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile  
20 25 30  
Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr  
35 40 45  
Leu Val Met Leu  
50

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 99 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys  
1 5 10 15  
Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile  
20 25 30  
Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val Ile Val Ile Thr  
35 40 45  
Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile His His Gly Val  
50 55 60  
Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys  
65 70 75 80  
Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln  
85 90 95

Met Gln Asn

(2) INFORMATION FOR SEQ ID NO:5:

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- (i) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 53 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe Arg His  
 1 5 10 15  
 Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe Ala Glu  
 20 25 30  
 Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly Gly  
 35 40 45  
 Val Val Ile Ala Thr  
 50

(2) INFORMATION FOR SEQ ID NO:6:

- (1) SEQUENCE CHARACTERISTICS:

  - (A) LENGTH: 45 amino acids
  - (B) TYPE: amino acid
  - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 1  
(D) OTHER INFORMATION: /note= "Xaa at position 1 corresponds to 1 or more APP amino acids which are not adjacent to B/A4 in nature."

(ix) FEATURE:

- (A) NAME/KEY: Modified-site  
(B) LOCATION: 45  
(D) OTHER INFORMATION: /note= "Xaa at position 45 corresponds to 1 or more APP amino acids which are not adjacent to B/A4 in nature."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Xaa Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln  
 1                   5                   10                   15  
 Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys Gly Ala Ile  
 20                   25                   30  
 Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Xaa  
 35                   40                   45

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: A4-0

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys  
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Ser Ala  
20 25

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: A4-P

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Gln Val His His Gln Lys  
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: A4-B

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val His His Gln Lys  
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
20 25

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 10 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:  
(B) CLONE: Opl

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr  
1 5 10

(2) INFORMATION FOR SEQ ID NO:11:

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## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3353 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 147..2234

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGTTTCCTCG GCAGCGGTAG GCGAGAGCAC GCGGAGGAGC GTGCGGGGG CCCCGGGAGA	60
CGGCGGGCGGT GGCGCGCGGG GCAGAGCAAG GACGCCGGCGG ATCCCACCTCG CACAGCAGCG	120
CACTCGGTGC CCCGCCAGG GTCGCG ATG CTG CCC GGT TTG GCA CTG CTC CTG Met Leu Pro Gly Leu Ala Leu Leu Leu	173
1 5	
CTG GCC GCC TGG ACG GCT CGG GCG CTG GAG GTA CCC ACT GAT GGT AAT Leu Ala Ala Trp Thr Ala Arg Ala Leu Glu Val Pro Thr Asp Gly Asn	221
10 15 20 25	
GCT GGC CTG CTG GCT GAA CCC CAG ATT GCC ATG TTC TGT GGC AGA CTG Ala Gly Leu Leu Ala Glu Pro Gln Ile Ala Met Phe Cys Gly Arg Leu	269
30 35 40	
AAC ATG CAC ATG AAT GTC CAG AAT GGG AAG TGG GAT TCA GAT CCA TCA Asn Met His Met Asn Val Gln Asn Gly Lys Trp Asp Ser Asp Pro Ser	317
45 50 55	
GGG ACC AAA ACC TGC ATT GAT ACC AAG GAA GGC ATC CTG CAG TAT TGC Gly Thr Lys Thr Cys Ile Asp Thr Lys Glu Gly Ile Leu Gln Tyr Cys	365
60 65 70	
CAA GAA GTC TAC CCT GAA CTG CAG ATC ACC AAT GTG GTA GAA GCC AAC Gln Glu Val Tyr Pro Glu Leu Gln Ile Thr Asn Val Val Glu Ala Asn	413
75 80 85	
CAG CCA GTG ACC ATC CAG AAC TGG TGC AAG CGG GGC CGC AAG CAG TGC Gln Pro Val Thr Ile Gln Asn Trp Cys Lys Arg Gly Arg Lys Gln Cys	461
90 95 100 105	
AAG ACC CAT CCC CAC TTT GTG ATT CCC TAC CGC TGC TTA GTT GGT GAG Lys Thr His Pro His Phe Val Ile Pro Tyr Arg Cys Leu Val Gly Glu	509
110 115 120	
TTT GTA AGT GAT GCC CTT CTC GTT CCT GAC AAG TGC AAA TTC TTA CAC Phe Val Ser Asp Ala Leu Leu Val Pro Asp Lys Cys Lys Phe Leu His	557
125 130 135	
CAG GAG AGG ATG GAT GTT TGC GAA ACT CAT CTT CAC TGG CAC ACC GTC Gln Glu Arg Met Asp Val Cys Glu Thr His Leu His Trp His Thr Val	605
140 145 150	
GCC AAA GAG ACA TGC AGT GAG AAG AGT ACC AAC TTG CAT GAC TAC GGC Ala Lys Glu Thr Cys Ser Glu Lys Ser Thr Asn Leu His Asp Tyr Gly	653
155 160 165	
ATG TTG CTG CCC TGC GGA ATT GAC AAG TTC CCA GGG GTA GAG TTT GTG Met Leu Leu Pro Cys Gly Ile Asp Lys Phe Arg Gly Val Glu Phe Val	701
170 175 180 185	
TGT TGC CCA CTG GCT GAA AA AGT GAC AAT GTG GAT TCT GCT GAT GCG	749

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Cys Cys Pro Leu Ala Glu Glu Ser Asp Asn Val Asp Ser Ala Asp Ala 190 195 200		
GAG GAG GAT GAC TCG GAT GTC TGG TGG GCC GGA GCA GAC ACA GAC TAT Glu Glu Asp Asp Ser Asp Val Trp Trp Gly Ala Asp Thr Asp Tyr 205 210 215	797	
GCA GAT GGG AGT GAA GAC AAA GTA GTA GAA GCA GAG GAG GAA GAA Ala Asp Gly Ser Glu Asp Lys Val Val Glu Val Ala Glu Glu Glu 220 225 230	845	
GTG GCT GAG GTG GAA GAA GAA GCC GAT GAT GAC GAG GAC GAT GAG Val Ala Glu Val Glu Glu Ala Asp Asp Asp Glu Asp Asp Glu 235 240 245	893	
GAT GGT GAT GAG GTA GAG GAA GAG GCT GAG GAA CCC TAC GAA GAA GCC Asp Gly Asp Glu Val Glu Glu Ala Glu Glu Pro Tyr Glu Glu Ala 250 255 260 265	941	
ACA GAG AGA ACC ACC AGC ATT GCC ACC ACC ACC ACC ACC ACA GAG Thr Glu Arg Thr Thr Ser Ile Ala Thr Thr Thr Thr Thr Glu 270 275 280	989	
TCT GTG GAA GAG GTG GTT CGA GTT CCT ACA ACA GCA GCC AGT ACC CCT Ser Val Glu Val Val Arg Val Pro Thr Thr Ala Ala Ser Thr Pro 285 290 295	1037	
GAT GCC GTT GAC AAG TAT CTC GAG ACA CCT GGG GAT GAG AAT GAA CAT Asp Ala Val Asp Lys Tyr Leu Glu Thr Pro Gly Asp Glu Asn Glu His 300 305 310	1085	
GCC CAT TTC CAG AAA GCC AAA GAG AGG CTT GAG GCC AAG CAC CGA GAG Ala His Phe Gln Lys Ala Lys Glu Arg Leu Glu Ala Lys His Arg Glu 315 320 325	1133	
AGA ATG TCC CAG GTC ATG AGA GAA TGG GAA GAG GCA GAA CGT CAA GCA Arg Met Ser Gln Val Met Arg Glu Trp Glu Ala Glu Arg Gln Ala 330 335 340 345	1181	
AAG AAC TTG CCT AAA GCT GAT AAG AAG GCA GTT ATC CAG CAT TTC CAG Lys Asn Leu Pro Lys Ala Asp Lys Ala Val Ile Gln His Phe Gln 350 355 360	1229	
GAG AAA GTG GAA TCT TTG GAA CAG GAA GCA GCC AAC GAG AGA CAG CAG Glu Lys Val Glu Ser Leu Glu Gln Glu Ala Ala Asn Glu Arg Gln Gln 365 370 375	1277	
CTG GTG GAG ACA CAC ATG GCC AGA GTG GAA GCC ATG CTC AAT GAC CGC Leu Val Glu Thr His Met Ala Arg Val Glu Ala Met Leu Asn Asp Arg 380 385 390	1325	
CGC CGC CTG GCC CTG GAG AAC TAC ATC ACC GCT CTG CAG GCT GTT CCT Arg Arg Leu Ala Leu Glu Asn Tyr Ile Thr Ala Leu Gln Ala Val Pro 395 400 405	1373	
CCT CGG CCT CGT CAC GTG TTC AAT ATG CTA AAG AAG TAT GTC CGC GCA Pro Arg Pro Arg His Val Phe Asn Met Leu Lys Lys Tyr Val Arg Ala 410 415 420 425	1421	
GAA CAG AAG GAC AGA CAG CAC ACC CTA AAG CAT TTC GAG CAT GTG CGC Glu Gln Lys Asp Arg Gln His Thr Leu Lys His Phe Glu His Val Arg 430 435 440	1469	
ATG GTG GAT CCC ARG AAA GCC GCT CAG ATC CGG TCC CAG GTT ATG ACA Met Val Asp Pro Lys Lys Ala Ala Gln Ile Arg Ser Gln Val Met Thr 445 450 455	1517	

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CAC CTC CGT GTG ATT TAT GAG CGC ATG AAT CAG TCT CTC TCC CTG CTC His Leu Arg Val Ile Tyr Glu Arg Met Asn Gln Ser Leu Ser Leu Leu 460 465 470	1565
TAC AAC GTG CCT GCA GTG GCC GAG GAG ATT CAG GAT GAA GTT GAT GAG Tyr Asn Val Pro Ala Val Ala Glu Glu Ile Gln Asp Glu Val Asp Glu 475 480 485	1613
CTG CTT CAG AAA GAG CAA AAC TAT TCA GAT GAC GTC TTG GCC AAC ATG Leu Leu Gln Lys Glu Gln Asn Tyr Ser Asp Asp Val Leu Ala Asn Met 490 495 500 505	1661
ATT AGT GAA CCA AGG ATC AGT TAC GGA AAC GAT GCT CTC ATG CCA TCT Ile Ser Glu Pro Arg Ile Ser Tyr Gly Asn Asp Ala Leu Met Pro Ser 510 515 520	1709
TTG ACC GAA ACG AAA ACC ACC GTG GAG CTC CTT CCC GTG AAT GGA GAG Leu Thr Glu Thr Lys Thr Val Glu Leu Leu Pro Val Asn Gly Glu 525 530 535	1757
TTC AGC CTG GAC GAT CTC CAG CCG TGG CAT TCT TTT GGG GCT GAC TCT Phe Ser Leu Asp Asp Leu Gln Pro Trp His Ser Phe Gly Ala Asp Ser 540 545 550	1805
GTC CCA GCC AAC ACA GAA AAC GAA GTT GAG CCT GTT GAT CCC CGC CCT Val Pro Ala Asn Thr Glu Asn Glu Val Pro Val Asp Ala Arg Pro 555 560 565	1853
GCT GCC GAC CGA CGA CTG ACC ACT CGA CCA GGT TCT GGG TTG ACA AAT Ala Ala Asp Arg Gly Leu Thr Thr Arg Pro Gly Ser Gly Leu Thr Asn 570 575 580 585	1901
ATC AAG ACG GAG GAG ATC TCT GAA GTG AAG ATG GAT GCA GAA TTC CGA Ile Lys Thr Glu Glu Ile Ser Glu Val Lys Met Asp Ala Glu Phe Arg 590 595 600	1949
CAT GAC TCA GGA TAT GAA GTT CAT CAT CAA AAA TTG GTG TTC TTT GCA His Asp Ser Gly Tyr Glu Val His His Gln Lys Leu Val Phe Phe Ala 605 610 615	1997
GAA GAT GTG GGT TCA AAC AAA GGT GCA ATC ATT GGA CTC ATG GTG GGC Glu Asp Val Gly Ser Asn Lys Gly Ala Ile Ile Gly Leu Met Val Gly 620 625 630	2045
GGT GTT GTC ATA GCG ACA GTG ATC GTC ATC ACC TTG GTG ATG CTG AAG Gly Val Val Ile Ala Thr Val Ile Ile Thr Leu Val Met Leu Lys 635 640 645	2093
AAG AAA CAG TAC ACA TCC ATT CAT CAT GGT GTG GTG GAG CTT GAC GCC Lys Lys Gln Tyr Thr Ser Ile His His Gly Val Val Glu Val Asp Ala 650 655 660 665	2141
GCT GTC ACC CCA GAG GAG CGC CAC CTG TCC AAG ATG CAG CAG AAC GGC Ala Val Thr Pro Glu Glu Arg His Leu Ser Lys Met Gln Gln Asn Gly 670 675 680	2189
TAC GAA AAT CCA ACC TAC AAG TTC TTT GAG CAG ATG CAG AAC TAGACCCCCG Tyr Glu Asn Pro Thr Tyr Lys Phe Phe Glu Gln Met Gln Asn 685 690 695	2241
CCACAGCAGC CTCTGAAGTT GGACAGCAAA ACCATTGCTT CACTACCCAT CGGTGTCCAT	2301
TTATAGAATA ATGTGGGAAG AAACAAACCC GTTTATGAT TTACTCATTA TCGCCTTTG	2361
ACAGCTGTGC TGTAAACACAA GTAGATGCCT GAACTTGAAT TAATCCACAC ATCAGTAATG	2421
TATTCTATCT CTCTTTACAT TTTGGTCTCT ATACTACATT ATTAATGGGT TTTGTGTACT	2481

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GTAAAGAATT TAGCTGTATC AAACTAGTGC ATGAATAGAT TCTCTCCTGA TTATTTATCA	2541
CATAGCCCT TAGCCAGTTG TATATTATTC TTGTGGTTG TGACCCAATT AAGTCCTACT	2601
TTACATATGC TTTAAGAACATC GATGGGGAT GCTTCATGTG AACGTGGGAG TTCAGCTGCT	2661
TCTCTGCCT AAGTATTCCCT TTCCATGATCA CTATGCATTT TAAAGTTAAA CATTTTAAG	2721
TATTCAGAT CCTTTAGAGA GATTTTTTT CCATGACTGC ATTTTACTGT ACAGATTGCT	2781
GCTTCTGCTA TATTTGTGAT ATAGGAATTAGAGATACA CACGTTGTT TCTTCGTGCC	2841
TCTTTATGT GCACACATTA GGCATTGAGA CTTCAAGCTT TTCTTTTT GTCCACGTAT	2901
CTTGGGTCT TTGATAAAGA AAAGAACCCC TGTTCAATTGTT AAGCACTTTT ACGGGGCGGG	2961
TGGGGAGGGG TGCTCTGCTG GTCTTCATT ACCAAGAATT CTCCAAAACA ATTTCTGCA	3021
GGATGATTGT ACAGAACAT TGCTTATGAC ATGATCGCTT TCTACACTGT ATTACATAAA	3081
TAAATTAAAT AAAATAACCC CGGGCAAGAC TTTTCTTGA AGGATGACTA CAGACATTAA	3141
ATAATCGAAG TAATTTGGG TGGGGAGGAAG AGGCAGATTCA ATTTTCTTT AACCAGTCTG	3201
AAGTTTCATT TATGATACAA AAGAAGATGA AAATGGAAGT GGCAATATAA GGGGATGAGG	3261
AAGGCATGCC TGGACAAACC CTTCTTTAA GATGTGTCTT CAATTTGTAT AAAATGGTGT	3321
TTTCATGTAA ATAAATACAT TCTTGGAGGA GC	3353

## (2) INFORMATION FOR SEQ ID NO:12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 695 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: protein

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Leu Pro Gly Leu Ala Leu Leu Leu Ala Ala Trp Thr Ala Arg			
1	5	10	15

Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro		
20	25	30

Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln		
35	40	45

Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp		
50	55	60

Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu			
65	70	75	80

Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn		
85	90	95

Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val		
100	105	110

Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu		
115	120	125

Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys	
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130	135	140													
Glu	Thr	His	Leu	His	Trp	His	Thr	Val	Ala	Lys	Glu	Thr	Cys	Ser	Glu
145										155					160
Lys	Ser	Thr	Asn	Leu	His	Asp	Tyr	Gly	Met	Leu	Leu	Pro	Cys	Gly	Ile
										165	170				175
Asp	Lys	Phe	Arg	Gly	Val	Glu	Phe	Val	Cys	Cys	Pro	Leu	Ala	Glu	Glu
										180	185				190
Ser	Asp	Asn	Val	Asp	Ser	Ala	Asp	Ala	Glu	Glu	Asp	Asp	Ser	Asp	Val
										195	200				205
Trp	Trp	Gly	Gly	Ala	Asp	Thr	Asp	Tyr	Ala	Asp	Gly	Ser	Glu	Asp	Lys
										210	215				220
Val	Val	Glu	Val	Ala	Glu	Glu	Glu	Glu	Val	Ala	Glu	Val	Glu	Glu	Glu
										225	230				240
Glu	Ala	Asp	Asp	Asp	Glu	Asp	Asp	Glu	Asp	Gly	Asp	Glu	Val	Glu	Glu
										245	250				255
Glu	Ala	Glu	Glu	Pro	Tyr	Glu	Glu	Ala	Thr	Glu	Arg	Thr	Thr	Ser	Ile
										260	265				270
Ala	Thr	Thr	Thr	Thr	Thr	Thr	Glu	Ser	Val	Glu	Glu	Val	Val	Arg	
										275	280				285
Val	Pro	Thr	Thr	Ala	Ala	Ser	Thr	Pro	Asp	Ala	Val	Asp	Lys	Tyr	Leu
										290	295				300
Glu	Thr	Pro	Gly	Asp	Glu	Asn	Glu	His	Ala	His	Phe	Gln	Lys	Ala	Lys
										305	310				320
Glu	Arg	Leu	Glu	Ala	Lys	His	Arg	Glu	Arg	Met	Ser	Gln	Val	Met	Arg
										325	330				335
Glu	Trp	Glu	Glu	Ala	Glu	Arg	Gln	Ala	Lys	Asn	Leu	Pro	Lys	Ala	Asp
										340	345				350
Lys	Lys	Ala	Val	Ile	Gln	His	Phe	Gln	Glu	Lys	Val	Glu	Ser	Leu	Glu
										355	360				365
Gln	Glu	Ala	Ala	Asn	Glu	Arg	Gln	Gln	Leu	Val	Glu	Thr	His	Met	Ala
										370	375				380
Arg	Val	Glu	Ala	Met	Leu	Asn	Asp	Arg	Arg	Arg	Leu	Ala	Leu	Glu	Asn
										385	390				400
Tyr	Ile	Thr	Ala	Leu	Gln	Ala	Val	Pro	Pro	Arg	Pro	Arg	His	Val	Phe
										405	410				415
Asn	Met	Leu	Lys	Lys	Tyr	Val	Arg	Ala	Glu	Gln	Lys	Asp	Arg	Gln	His
										420	425				430
Thr	Leu	Lys	His	Phe	Glu	His	Val	Arg	Met	Val	Asp	Pro	Lys	Lys	Ala
										435	440				445
Ala	Gln	Ile	Arg	Ser	Gln	Val	Met	Thr	His	Leu	Arg	Val	Ile	Tyr	Glu
										450	455				460
Arg	Met	Asn	Gln	Ser	Leu	Ser	Leu	Leu	Tyr	Asn	Val	Pro	Ala	Val	Ala
										465	470				480
Glu	Glu	Ile	Gln	Asp	Glu	Val	Asp	Glu	Leu	Leu	Gln	Lys	Glu	Gln	Asn
										485	490				495

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Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser  
500 505 510  
Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr  
515 520 525  
Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln  
530 535 540  
Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn  
545 550 555 560  
Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr  
565 570 575  
Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser  
580 585 590  
Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val  
595 600 605  
His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys  
610 615 620  
Gly Ala Ile Ile Gly Leu Met Val Gly Val Val Ile Ala Thr Val  
625 630 635 640  
Ile Val Ile Thr Leu Val Met Leu Lys Lys Gln Tyr Thr Ser Ile  
645 650 655  
His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg  
660 665 670  
His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys  
675 680 685  
Phe Phe Glu Gln Met Gln Asn  
690 695

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 amino acids  
(B) TYPE: amino acid  
(D) TOPOLOGY: linear

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 11  
(D) OTHER INFORMATION: /note= ""Xaa at Position 11 is  
either Glu or Gln.""

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 27  
(D) OTHER INFORMATION: /note= ""Xaa at position 27 is  
either Ser or Asn.""

(ix) FEATURE:  
(A) NAME/KEY: Modified-site  
(B) LOCATION: 28  
(D) OTHER INFORMATION: /not = ""Xaa at position 28 is  
either Ala or Lys.""

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Xaa Val His His Gln Lys  
1 5 10 15

Leu Val Phe Phe Ala Glu Asp Val Gly Ser Xaa Xaa  
20 25

What Is Claimed Is:

1. An amyloid binding composition for *in vivo* imaging of amyloid deposits comprising:

(a) a labeled amyloid protein or variant thereof that binds to amyloid deposits *in vivo*; and  
(b) a pharmaceutically acceptable carrier.

2. The composition of claim 1, wherein said amyloid protein is  $\beta$ -amyloid polypeptide or a variant thereof.

3. The composition of claim 2, wherein said  $\beta$ -amyloid polypeptide variant has the following amino acid sequence (SEQ ID NO:13):

N-Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-X-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Y1-Y2-COOH;

wherein X is either Glu or Gln; Y1 is either Ser or Asn; and Y2 is either Ala or Lys.

4. The composition of claim 3, wherein said  $\beta$ -amyloid polypeptide variant is selected from the group consisting of (1) a variant wherein when X is Glu, Y1 is Ser and Y2 is Ala, (2) a variant wherein when X is Glu, Y1 is Asn and Y2 is Lys, and (3) a variant wherein when X is Gln, Y1 is Asn and Y2 is Lys.

5. The composition of claim 2, wherein said  $\beta$ -amyloid polypeptide or variant thereof has an amino acid sequence selected from the following group of amino acid sequences:

(A) (SEQ ID NO:2) Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-Glu-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met-Val-Gly-Gly-Val-Val-Ile-Ala-Thr;

(B) (SEQ ID NO:3) Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-Tyr-Glu-Val-His-His-Gln-Lys-Leu-Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met-Val-

Gly-Gly-Val-Val-Ile-Ala-Thr-Val-Ile-  
Val-Ile-Thr-Leu-Val-Met-Leu;  
(C) (SEQ ID NO:4) Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-Gly-  
Tyr-Glu-Val-His-His-Gln-Lys-Leu-Val-  
Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-Asn-  
Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met-Val-  
Gly-Gly-Val-Val-Ile-Ala-Thr-Val-Ile-  
Val-Ile-Thr-Leu-Val-Met-Leu-Lys-Lys-  
Lys-Gln-Tyr-Thr-Ser-Ile-His-His-Gly-  
Val-Val-Glu-Val-Asp-Ala-Ala-Val-Thr-  
Pro-Glu-Glu-Arg-His-Leu-Ser-Lys-Met-  
Gln-Gln-Asn-Gly-Tyr-Glu-Asn-Pro-Thr-  
Tyr-Lys-Phe-Phe-Glu-Gln-Met-Gln-Asn;  
(D) (SEQ ID NO:5) Lys-Thr-Glu-Glu-Ile-Ser-Glu-Val-Lys-  
Met-Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-  
Gly-Tyr-Glu-Val-His-His-Gln-Lys-Leu-  
Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-  
Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met-  
Val-Gly-Gly-Val-Val-Ile-Ala-Thr;  
(E) (SEQ ID NO:6) X-Asp-Ala-Glu-Phe-Arg-His-Asp-Ser-  
Gly-Tyr-Glu-Val-His-His-Gln-Lys-Leu-  
Val-Phe-Phe-Ala-Glu-Asp-Val-Gly-Ser-  
Asn-Lys-Gly-Ala-Ile-Ile-Gly-Leu-Met-  
Val-Gly-Gly-Val-Val-Ile-Ala-Thr-Y,

wherein X and Y are one or more APP amino acids which are  
not adjacent to  $\beta$ /A4 in the nature;

and

(F) any fragment of (A)-(E), wherein said fragment is  
large enough to bind amyloid deposit *in vivo*.

6. The composition of claim 1, wherein said labeled  
amyloid protein is radiolabeled amyloid protein.

7. The composition of claim 1, wherein said  
radiolabeled amyloid protein is Technetium 99m-labeled  
amyloid protein.

8. An *in vivo* method for detecting amyloid dep sites  
in a subject comprising the steps of

(a) administering to a subject a detectable quantity of an amyloid binding composition comprising a labeled amyloid protein or variant thereof and a pharmaceutically acceptable carrier; and

(b) detecting the binding of the labeled protein or variant thereof to the amyloid deposit.

9. The method of claim 8, wherein said amyloid protein is the  $\beta$ -amyloid polypeptide or variant thereof.

10. The method of claim 8, wherein said amyloid protein is radiolabeled.

11. The method of claim 10, wherein said detecting involves radioactive imaging.

12. The method of claim 8, wherein said administering is selected from the group consisting of intravenous injection, intraventricular injection and a combination of both intravenous and intraventricular injection.

13. The method of claim 8, wherein said amyloid deposits are located in the brain of a subject.

14. A method of diagnosing an amyloidosis-associated disease by detecting amyloid deposits in a subject suspected of having amyloid deposits, said method comprising the steps of:

(a) administering to a subject a detectable quantity of an amyloid binding composition comprising a labeled amyloid protein or variant thereof and a pharmaceutically acceptable carrier; and

(b) detecting the binding of said labeled protein to said amyloid deposit.

15. The method of claim 14, wherein said amyloidosis-associated disease is selected from the group consisting of Alzheimer's Disease and Down Syndrome.

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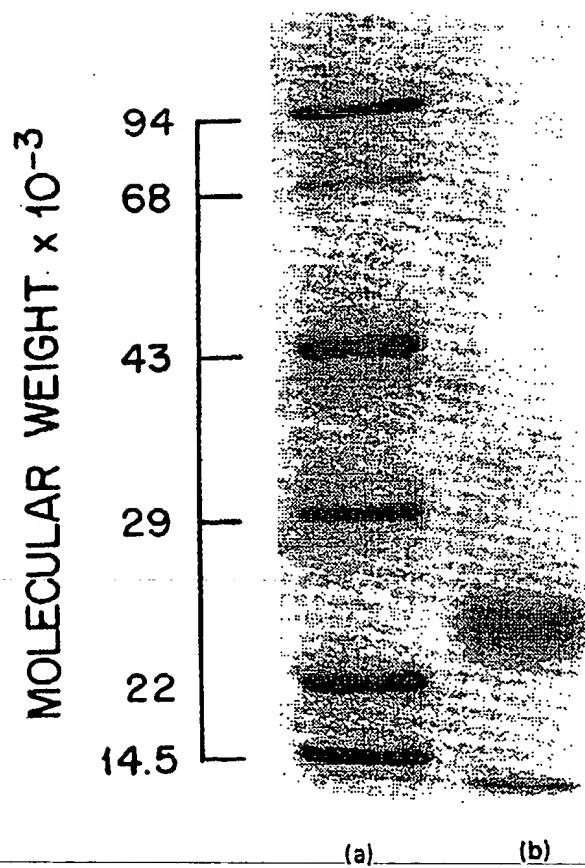
**FIG. 1**

Clinical Association	Notation	Protein Type
<b>ACQUIRED SYSTEMIC AMYLOIDOSIS</b>		
Immunoglobulin light-chain (primary),	AL	Light chain, type subtype
Multiple myeloma		
Reactive (secondary)	AA	Protein A
Hemodialysis amyloidosis	AH	$\beta_2$ microglobulin
<b>HEREDOFAMILIAL</b>		
Polyneuropathy	AF	Prealbumin, variant
Familial Mediterranean fever	AA	Protein A
<b>ORGAN-LIMITED</b>		
Hereditary Icelandic Congophilic angiopathy	ACv <sub>C</sub>	Cystatin C, variant
Alzheimer's disease: vessels and plaques	ACv <sub>B1</sub>	$\beta$ protein
Senile cardiac	ACp <sub>B</sub>	
<b>LOCALIZED ENDOCRINE</b>		
Pancreatic islet	AE <sub>f</sub>	Islet amyloid protein [IAP]
Medullary thyroid carcinoma	AE <sub>t</sub>	Precalcitonin

**SUBSTITUTE SHEET (RULE 26)**

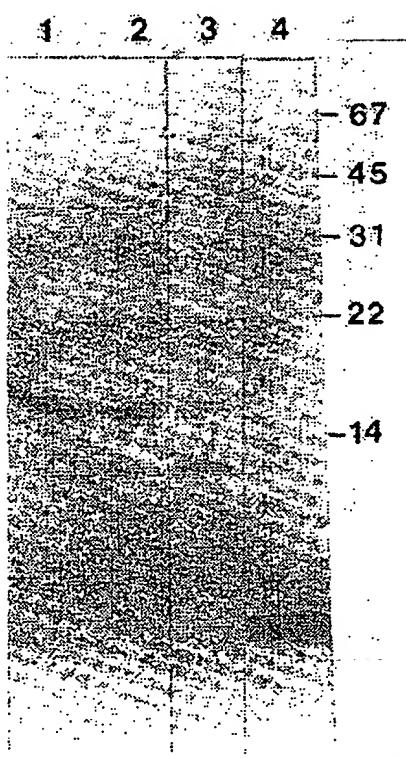
2/10

FIG. 2



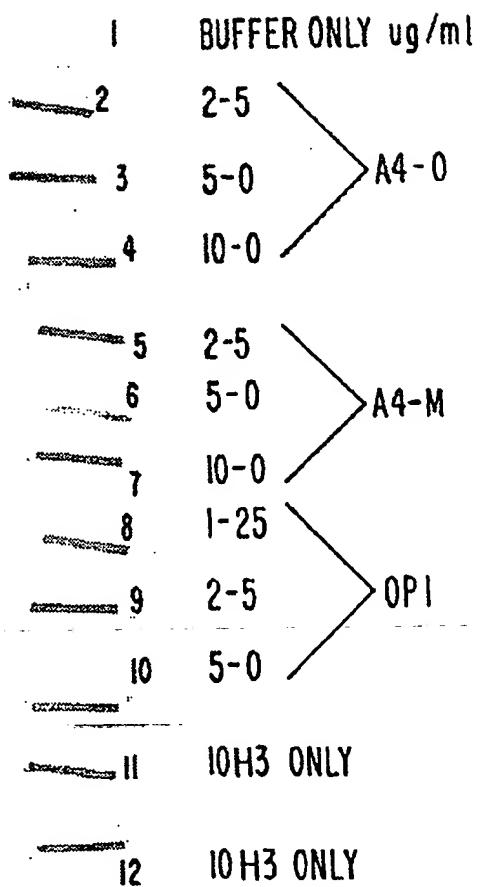
SUBSTITUTE SHEET (RULE 26)

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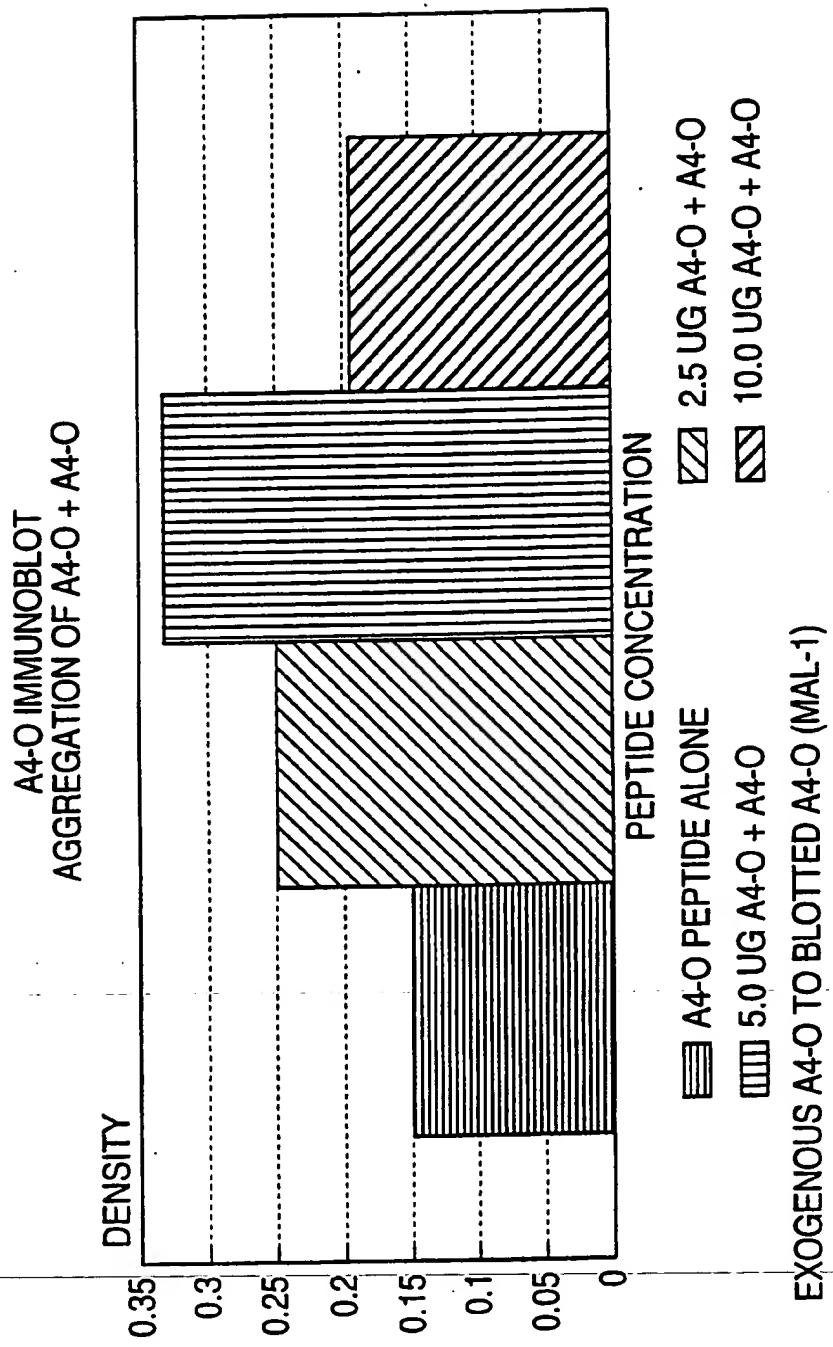
**FIG. 3**

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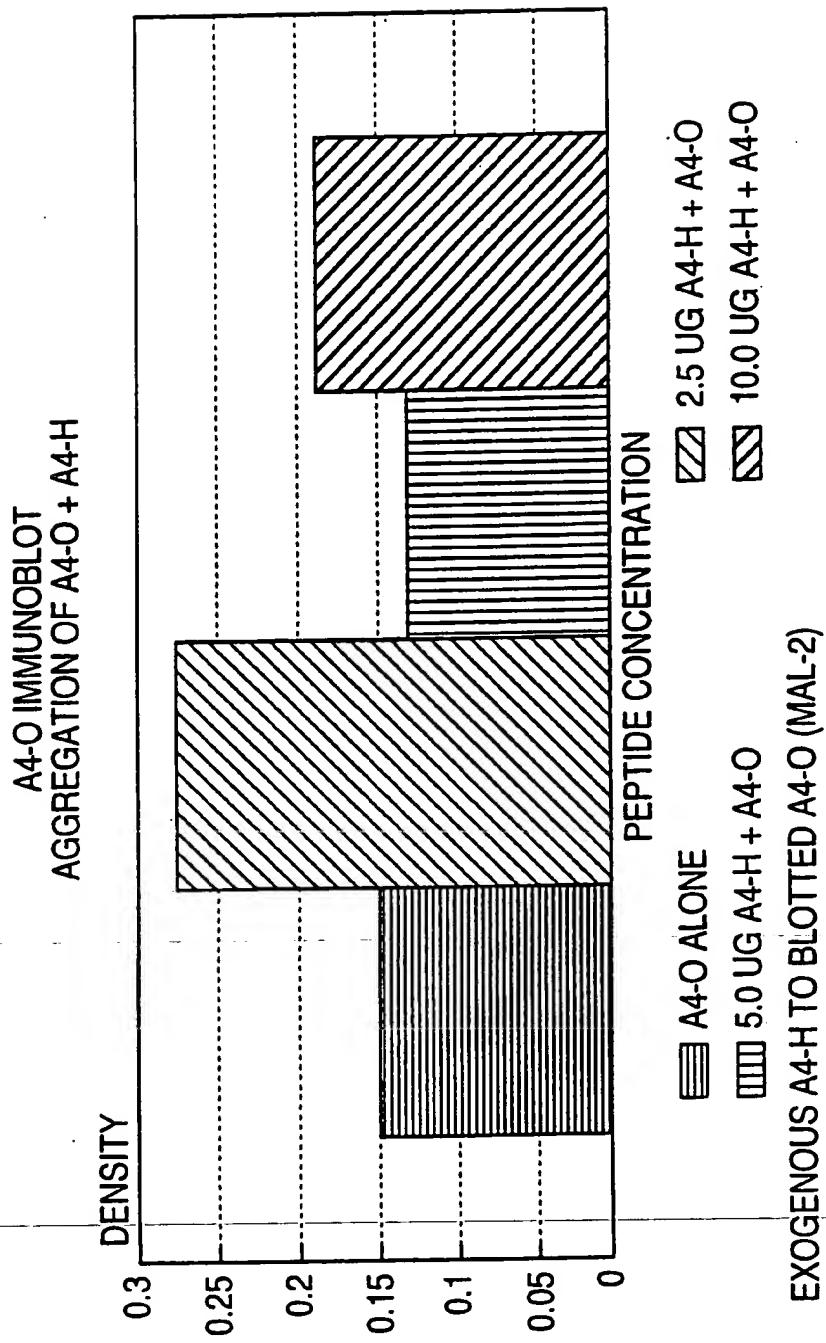
## FIG. 4



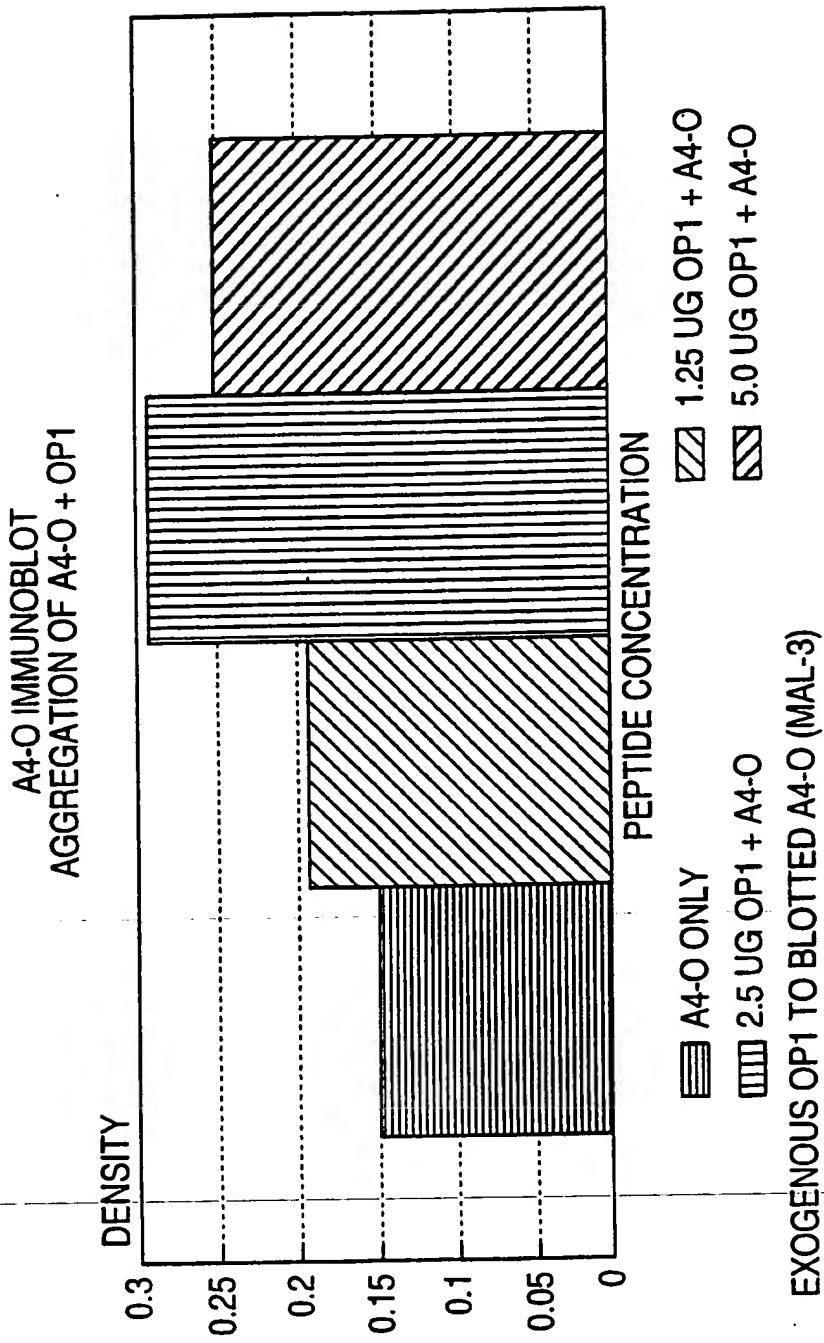
5/10

**FIG. 5****SUBSTITUTE SHEET (RULE 26)**

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**FIG. 6****SUBSTITUTE SHEET (RULE 26)**

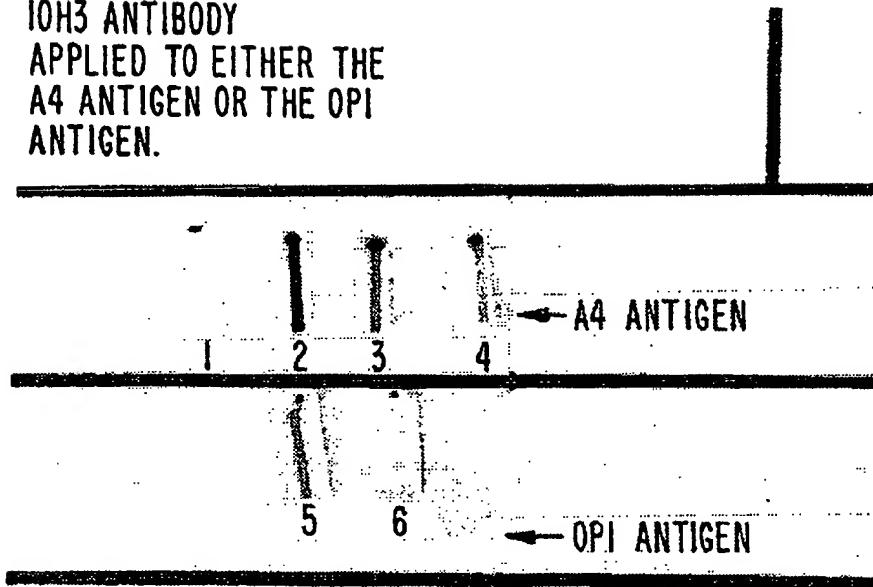
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**FIG. 7****SUBSTITUTE SHEET (RULE 26)**

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**FIG. 8**

10H3 ANTIBODY  
APPLIED TO EITHER THE  
A4 ANTIGEN OR THE OPI  
ANTIGEN.



**FIG. 9A**

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AGTTTCCTCGGCAGCGGTAGGCGAGA -121

2 GCACGCGGAGGAGCGTGCAGGGCCCCGGGAGACGGCGCGTGGCGCGCAGAG -61

3 CAAGGACGCGCGGATCCCACTCGCACAGCAGCGACTCGTGCAGGGCGCTGGAGGTA -1

4 ATGCTGCCCGTTGGCACTGCTCCTGCTGGCCGCTGGACGGCTGGCGCTGGAGGTA 60  
M L P G L A L L L A A W T A R A L E V  
10 20  
1

5 CCCACTGATGGTAATGCTGGCTGCTGGCTGAACCCAGATTGCCATGTTCTGGCAGA 120  
P T D G N A G L L A E P Q I A M F C G R  
30 40

6 CTGAACATGCACATGAATGTCCAGAATGGGAACTGGGATTAGATCCATCAGGGACAAA 180  
L N M H M N V Q N G K W D S D P S G T K  
50 60

7 ACCTGCATTGATACCAAGGAAGGCATCCTGCAGTATTGCCAAGAAGTCTACCCCTGAAC 240  
T C I D T K E G I L Q Y C Q E V Y P E L  
70 80

8 CAGATCACCAATGTGGTAGAACGCAACCAACCGAGTGACCATCCAGAACTGGTGCAGCGG 300  
Q I T N V V E A N O P V T I Q N W C K R  
90 100

9 GGCGCAAGCAGTGCAAGACCCATCCCCACTTGTGATTCCTACCGCTGCTAGTTGGT 360  
G R K Q C K T H P H F V I P Y R C L V G  
110 120

10 GAGTTGTAAAGTGTGATGCCCTCTCGTCTGACAAGTGCACAAATTCTACACCAGGAGGG 420  
E F V S D A L L V P D K C K F L H Q E R  
130 140

11 ATGGATGTTGCGAAACTCATCTCACTGGCACACCGTCGCCAAAGAGACATGCAGTGAG 480  
M D V C E T H L H W H T V A K E T C S E  
150 160

12 AAGAGTACCAACTTGCATGACTACGGCATGTTGCTGCCCTGCCGAAATTGACAAGTCCGA 540  
K S T N L H D Y G M L L P C G I D K F R  
170 180

13 GGGTAGAGTTGTGTTGCCACTGGCTGAAGAAAGTACAATGTGGATTCTGCTGAT 600  
G V E F V C C P L A E E S D N V D S A D  
190 200

14 GCGGAGGAGGATGACTCGGATGTTGGGGCGGAGCAGACACAGACTATGCAGATGGG 660  
A E E D D S D V W W G G A D T D Y A D G  
210 220

15 AGTGAAGACAAAGTAGTAGAAGTAGCAGAGGGAGGAAGAAGTGGCTGAGGTGGAAGAAGAA 720  
S E D K V V E V A E E E E V A E V E E E  
230 240

16 GAAGCCGATGATGACCGAGGACATGAGGATGGTGTGAGGTAGAGGAAGAGGCTGAGGAA 780  
E A D D D E D D E D G D E V E E A E E  
250 260

17 CCCTACGAAGAACCCACAGAGAGAACCAACCAAGATTGCCACCACCAACCAACACA 840  
P Y E E A T E R T T S I A T T T T T T T  
270 280

18 GAGTCTGTGGAAGAGGTGGTTCGAGTTCTACACAGCAGCCAGTACCCCTGATGCCGTT 900  
E S V E E V V R V P T T A A S T P D A V  
290 300

19 GACAAGTATCTCGAGACACCTGGGATGAGAATGAAACATGCCATTCCAGAAAGCCAA 960  
D K Y L E T P G D E N E H A H F Q K A K  
310 320

20 GAGAGGCTTGAGGCCAAGCACCGAGAGAGAATGICCCAGGTATGAGAGAATGGAGAG 1020  
E R L E A K H R E R M S Q V M R E W E E  
330 340

21 GCAGAACGTCAGCAAAGAACTTGCCTAAAGCTGATAAGAACGGCAGTTATCCAGCATTTC 1080  
A E R Q A K N L P K A D K K A V I Q H F  
350 360

---

22 CAGGAGAAAGTGAATCTTGGAACAGGAAGCAGCCAAAGCAGAGAGACAGCAGCTGGTGGAG 1140  
Q E K V E S L E Q E A A N E R Q Q L V E  
370 380

23 ACACACATGGCCAGAGTGGAGGCCATGCTCAATGACCCGCCCTGGCCCTGGAGAAC 1200  
T H M A R V E A M L N D R R R L A L E N  
390 400

24 TACATCACCGCTCTGCAGGCTGTTCTCGGCCCTGTCACGTGTTCAATATGCTAAAG 1260  
Y I T A L Q A V P P R P R H V F N M L K  
410 420

25 AAGTATGTCCGCGCAGAACAGAAGGACAGACAGCACACCTAAAGCATTTCGAGCATGTG 1320  
C Y V R A E Q K D R Q H T L K H F E H V  
430 440

**SUBSTITUTE SHEET (RULE 26)**

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**FIG. 9B**

26 CGCATGGTGGATCCCAAGAAAGCCGCTCAGATCCGGTCCCAGGTTATGACACACCTCCGT 1380  
 R M V D P K K A A Q I R S Q V M T M L R  
 450 460  
 27 GTGATTATGAGCGCATGAATCAGTCTCTCCCTGCCTACAACGTGCCCTGCAGTGGCC 1440  
 V I Y E R M N Q S L S L L Y N V P A V A  
 470 480  
 28 GAGGAGATTCAAGGATGAAGTTGATGAGCTGCTTCAGAAAAGAGCAAACATTACAGATGAC 1500  
 E E I Q D E V D E L L Q K E Q N Y S D D  
 490 500  
 29 GTCTGGCCAACATGATTAGTGAACCAAGGATCAGTTACGGAAACGATGCTCTCATGCCA 1560  
 V L A N M I S E P R I S Y G N D A L M P  
 510 520  
 30 TCTTGACCGAAACGAAAACCACCGTGGAGCTCCTCCCGTGAATGGAGAGTCAGCCTG 1620  
 S L T E T K T T V E L L P V N G E F S L  
 530 540  
 31 GACGATCTCCAGCCGTGGATTCTTTGGGGCTGACTCTGTGCCAGCCAACACAGAAAAC 1680  
 D D L Q P W H S F G A D S V P A N T E N  
 550 560  
 32 GAAGTTGAGCCTGTTGATGCCGCCCTGCTGCCGACCGAGGACTGACCAACTCGACCAGGT 1740  
 E V E P V D A R P A A D R G L T T R P G  
 570 580  
 33 TCTGGGTGACAAATATCAAGACGGAGGAGTCCTGAAGTGAAGATGGATGCAGAACATT 1800  
 S G L T N I K T E E I S E V K M D A E F  
 590 600  
 34 CGACATGACTCAGGATATGAAGTTCATCATCAAAATTGGTGTCTTGAGAACATGTG 1860  
 R H D S G Y E V H H O K L V F F A E D V  
 610 620  
 35 GGTCAAACAAAGGTGCAATCATTGGACTCATGGTGGCGGTGTGTCAAGTCAGCAGTG 1920  
 G S N K G A I I G L M V G G V V I A T V  
 630 640  
 36 ATCGTCATCACCTGGTGAATGCTGAAGAAGAACAGTACACATCATTATGGTGTG 1980  
 I V I T L V M L K K Q Y T S I H H G V  
 650 660  
 37 GTGGAGGTTGACGCCGCTGTCACCCCCAGAGGGAGCGCCACCTGTCAAGATGCAGAAC 2040  
 V E V D A A V T P E E R H L S K M Q Q N  
 670 680  
 38 GGCTACGAAAATCCAACCTACAAGTTCTTGAGCAGATGCAGAACTAGACCCCCGCCACA 2100  
 G Y E N P T Y K F F E Q M Q N \*  
 690  
 39 GCAGCCTCTGAAGTGGACAGCAAAACCATTGCTTCACTACCCATCGGTGCCATTATA 2160  
 40 GAATAATGTGGGAAGAAACAAACCCGTTTATGATTTACTCATTATGCCCTTGACAGC 2220  
 41 TGTGCTGTAACACAAGTAGATGCCCTGAACCTGAATTAAATCCACACATCAGTAATGTATT 2280  
 42 TATCTCTTTACATTGGTCTCTATACTACATTATAATGGGTTTGTGTACTGTAAA 2340  
 43 GAATTAGCTGTATCAAACTAGTCATGAATAGATTCTCCTGTGATTATTTACACATAG 2400  
 44 CCCCTTAGCCAGTTGTATATTATTCTGGTTGTGACCCAATTAAGTCTACTTTACA 2460  
 45 TATGCTTAAGAATCGATGGGGATGCTCATGTGAACGTGGAGTCAGCTGTTCTCT 2520  
 46 TGCCTAAGTATTCCCTTCTGATCACTATGCATTAAAGTTAACATTAAAGTATT 2580  
 47 CAGATGCTTAGAGAGATTTTTCCATGACTGCATTACTGTACAGATGCTGCTTC 2640  
 48 TGCTATATTGTGATAGGAATTAAGAGGATACACAGTTGTTCTCGTGCCTGTT 2700  
 49 TATGTGCACACATTAGGCATTGAGACTTCAGCTTTCTTTGTCCACGTATTTG 2760  
 50 GGTCTTGATAAAGAAAAGAATCCCTGTTCAATTGTAAAGCACTTTACGGGGGGGGGG 2820  
 51 AGGGGTGCTCTGCTGGTCTTCATTACCAAGAATTCTCCAAAACAATTTCCTGCAGGATG 2880  
 52 ATTGTACAGAACATTGCTTATGACATGATCGCTTCTACACTGTATTACATAATAAT 2940  
 53 TAAATAAAATAACCCGGGCAAGACTTTCTTGAAGGGATGACTACAGACATTAAATAAT 3000  
 54 CGAAGTAATTGGTGGGGAGAAGAGGAGATTCAATTTCCTTAACCAGTCTGAAGTT 3060  
 55 TCATTTATGATACAAAAGAAGATGAAAATGGAAGTGGCAATATAAGGGGATGAGGAAGGC 3120  
 56 ATGCCTGGACAAACCCCTCTTTAAGATGTGTCTCAATTGTATAAAATGGTGTGTTCA 3180  
 57 TGTAAATAAAATACATTCTGGAGGAGC-poly(A) tail

## INTERNATIONAL SEARCH REPORT

I National application No.  
PCT/US94/05809

## A. CLASSIFICATION OF SUBJECT MATTER

IPC(5) :G01N 33/367; A61K 49/00, 43/00

US CL :435/7.21; 424/1.11, 1.57, 9; 514/2

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/7.1, 7.2, 7.21; 424/1.11, 1.57, 1.69, 9; 514/2

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

Medline, EMBASE, BIOSIS, CA Search, WPO, APS, IntelliGenetics

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO, A, 93/04194 (MAGGIO ET AL) 04 March 1993, see entire document, especially page 4, lines 8-15, page 8, lines 14-17, page 12, lines 15-39 and page 14, lines 26-36.	1, 2, 6, 7, 8-15 3-5
Y	Proceedings of the National Academy of Science USA, Volume 87, issued June 1992, Maggio et al, "Reversible in vitro growth of Alzheimer disease beta-amyloid plaques by deposition of labeled amyloid peptide", pages 5462-5466, especially see Abstract on page 5462.	1-15

Further documents are listed in the continuation of Box C.  See patent family annex.

* Special categories of cited documents:	"T"	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
*'A'		document defining the general state of the art which is not considered to be of particular relevance
*'E'		earlier document published on or after the international filing date
*'L'		document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
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	"X"	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
	"Y"	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
	"A"	document member of the same patent family

Date of the actual completion of the international search

24 AUGUST 1994

Date of mailing of the international search report

SEP 06 1994

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## INTERNATIONAL SEARCH REPORT

I National application No.  
PCT/US94/05809

## C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X Y	Society for Neuroscience Abstracts from the 21st Annual Meeting, Volume 17, Number 1-2, issued Nov. 1991, Mantyh et al, "Distribution and Characterization of Amyloid Beta Protein Deposition in Normal Human and Alzheimer's Diseased Cerebral Cortex Using <sup>125</sup> I-BAP as the Radioligand", page 912, Abstract 364.4, see entire abstract.	1, 2, 6, 7 3-5, 8-15
Y	Nature, Volume 325, issued 19 February 1987, Kang et al "The precursor of Alzheimer's disease amyloid A4 protein resembles a cell-surface receptor", pages 733-735, especially see Fig. 2.	1-15
A	Freeman et al, editors, Physician Desk Reference For Radiology and Nuclear Medicine, published 1977 by Medical Economics Company, Oradell, N.J., pages 39-43.	1-15
A	Proceedings of the National Academy of Science USA, Volume 88, issued August 1991, Kowall et al, "An in vivo model for the neurodegenerative effects of beta amyloid and protection by substance P", pages 7247-7251.	1-15
A	Neurobiology of Aging, Volume 13, Number 5, issued 1992, May et al, "Beta-Amyloid Peptide In Vitro Toxicity: Lot-to-Lot Variability", pages 605-607.	1-15